

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:56:50 ; Search time 55 Seconds
(without alignments)
292.971 Million cell updates/sec

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Perfect score: 123

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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12	93	75.6	123	11	US-09-855-632-2
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19	15	12.2	15	9	US-09-564-329A-18	Sequence 18, Appli
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ALIGNMENTS

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; Patent No. US20020058241A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/934,586A
; FILING DATE: 23-Aug-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/225,080
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single


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; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; US-09-934-773-6

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; Sequence 2, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
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; US-09-963-620-6

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; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Safran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
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; PRIOR FILING DATE: 1998-12-02
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; PRIOR FILING DATE: 1999-02-17
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; US-09-963-620-6

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LOCATION: (50)..(64)
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; Publication No. US20030113818A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
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; PRIOR FILING DATE: 1997-03-10
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; PRIOR FILING DATE: 1998-01-12
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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
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; PRIOR FILING DATE: 1998-12-02
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; PRIOR APPLICATION NUMBER: 09/308,503
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LENGTH: 123

TYPE: PRT

ORGANISM: HUMAN PSCA (hPSCA)

FEATURE:

NAME/KEY: SITE

LOCATION: (50)..(64)

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LOCATION: (67)..(81)

US-09-855-632-2

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; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,632
; CURRENT FILING DATE: 2001-05-14
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LENGTH: 123

TYPE: PRT

ORGANISM: HUMAN PSCA (hPSCA)

US-09-855-632-6

Query Match 75.6%; Score 93; DB 11; Length 123;

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RESULT 14

US-10-224-720-2

; Sequence 2, Application US/10224720

; Publication No. US20030147806A1

; GENERAL INFORMATION:

; APPLICANT: Reiter, Robert E.

; APPLICANT: Witte, Owen N.

; APPLICANT: Saffran, Douglas C.

; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

; FILE REFERENCE: 30435.54US14

; CURRENT APPLICATION NUMBER: US/10/224,720

; CURRENT FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: US/09/359,326

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 08/814,279

; PRIOR FILING DATE: 1997-03-10

; PRIOR APPLICATION NUMBER: 60/071,141

; PRIOR FILING DATE: 1998-01-12

; PRIOR APPLICATION NUMBER: 60/074,675

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: 60/113,230

; PRIOR FILING DATE: 1998-12-21

; PRIOR APPLICATION NUMBER: 60/120,536

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; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)..(81)
; US-10-224-720-2

Query Match      75.6%; Score 93; DB 12; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.3e-77;
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; Sequence 6, Application US/10224720
; Publication No. US20030147806A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
; CURRENT FILING DATE: 2002-08-20
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
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; PRIOR FILING DATE: 1998-01-12
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; PRIOR APPLICATION NUMBER: 60/124,658
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; PRIOR APPLICATION NUMBER: 09/038,261
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; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
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; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; US-10-224-720-6

Query Match      75.6%; Score 93; DB 12; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.3e-77;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 56 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 19:52:00 ; Search time 40 Seconds
(without alignments)
295.719 Million cell updates/sec

Title: US-09-934-586A-2

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Gapop 60.0 , Gapext 60.0

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Maximum DB seq length: 2009000000

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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6	8	6.5	501	2 JH0447	alpha-1A-adrenergi
7	8	6.5	560	2 A38731	alpha-1A-adrenergi
8	8	6.5	572	2 I39369	alpha-1A-adrenergi
9	7	5.7	88	2 T08512	trbO protein - Ent
10	7	5.7	123	2 S29714	guanine-nucleotide
11	7	5.7	123	2 I52427	guanine-nucleotide
12	7	5.7	123	2 P82716	hypothetical prote
13	7	5.7	145	2 T32693	hypothetical prote
14	7	5.7	150	2 E87507	hypothetical prote
15	7	5.7	166	2 T48784	hypothetical prote
16	7	5.7	173	2 A95864	hypothetical prote
17	7	5.7	191	2 F72277	hypothetical prote
18	7	5.7	193	2 G69707	signal peptidase I
19	7	5.7	198	2 A75270	conserved hypochet
20	7	5.7	206	1 TVH0HS	fibroblast growth
21	7	5.7	206	2 T25161	hypothetical prote
22	7	5.7	213	2 H88469	protein C28H8.4 [i
23	7	5.7	213	2 T30618	hypothetical prote
24	7	5.7	252	1 S55288	phosphoglycolate p
25	7	5.7	252	2 A86003	phosphoglycolate p
26	7	5.7	252	2 C91157	phosphoglycolate p
27	7	5.7	252	2 AH1000	phosphoglycolate p
28	7	5.7	255	2 T36243	probable precorrin
29	7	5.7	273	2 A97359	hypothetical 30.3K

30 7 5.7 273 2 AB2577 conserved hypochet
31 7 5.7 287 2 G69766 conserved hypochet
32 7 5.7 290 2 C48547 nonstructural prot
33 7 5.7 291 2 AG1846 sulfate transport
34 7 5.7 291 2 B95316 probable ABC trans
35 7 5.7 296 2 A83109 hypothetical prote
36 7 5.7 296 2 H75439 probable antibioti
37 7 5.7 303 2 AH2295 hypothetical prote
38 7 5.7 329 2 AH3121 conserved hypochet
39 7 5.7 329 2 G98165 hypothetical prote
40 7 5.7 345 2 A70664 hypothetical prote
41 7 5.7 346 2 AB2129 iron(III) dicitrat
42 7 5.7 349 2 A70849 probable ABC-trans
43 7 5.7 354 2 A83059 probable hemin deg
44 7 5.7 362 2 B70876 probable transamin
45 7 5.7 365 2 G72306 conserved hypochet

ALIGNMENTS

RESULT 1

D48909

G protein-coupled receptor Gpcr8 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 19-May-2000

C;Accession: D48909

R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G

Genomics 18, 175-184, 1993

A;Title: Identification, chromosomal location, and genome organization of mammalian G-pro

A;Reference number: A48909; MUID:94116980; PMID:8288218

A;Accession: D48909

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-161 <WIL>

A;Cross-references: GB:L20333

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 6.5%; Score 8; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAIALL 110

Db 18 AAAIALL 25

RESULT 2

JN0831

GlnR protein - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000

C;Accession: JN0831

R;Wray Jr., L.V.; Fisher, S.H.

Gene 130, 145-150, 1993

A;Title: The Streptomyces coelicolor glnR gene encodes a protein similar to other bacter

A;Reference number: JN0831; MUID:93345814; PMID:7688332

A;Accession: JN0831

A;Molecule type: DNA

A;Residues: 1-267 <WRA>

A;Cross-references: GB:L03213; NID:g153282; PIDN:AAA02838.1; PID:g153283

C;Comment: This protein positively regulates the transcription of Glutamine synthetase.

C;Comment: This protein is a member of the sub-family of response regulator proteins.

C;Genetics:

A;Gene: glnR

C;Superfamily: response regulator homology

C;Keywords: DNA binding; phosphoprotein; transcription regulation

Query Match 6.5%; Score 8; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LPAIGLLL 117
 Db 18 LPAIGLLL 25

 RESULT 3
 T23158
 hypothetical protein K01A6.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T23158
 R:Cottage, A.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19701
 A:Accession: T23158
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-284 <WIL>
 A:Cross-references: EMBL:Z68750; PIDN:CAA92963.1; GSPDB:GNO0022; CESP:K01A6.4
 A:Experimental source: clone K01A6
 C:Genetics:
 A:Gene: CESP:K01A6.4
 A:Map position: 4
 A:Introns: 89/3; 104/3; 126/3
 C:Superfamily: Phaseolus glycine-rich cell wall protein 1.8

 Query Match 6.5%; Score 8; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 5.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

 Qy 2 KAVLLALL 9
 Db 4 KAVLLALL 11

 RESULT 4
 AF3509
 ATP/GTP-binding protein BMEI2060 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
 C:Accession: AF3509
 R:DelVecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Golsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesee
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: ADJ252; PMID:1175668
 A:Accession: AF3509
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-299 <KUP>
 A:Cross-references: GB:AE008917; PIDN:AAU53241.1; PID:gl7984119; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI2060
 A:Map position: 1
 C:Superfamily: ydia protein

 Query Match 6.5%; Score 8; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

 Qy 103 AAAILALL 110
 Db 282 AAAILALL 289

 RESULT 5
 H75060
 hydrogenase (EC 1.-.-.-) 4 component D PAB1391 [imported] - Pyrococcus abyssi (strain O4
 C:Species: Pyrococcus abyssi
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: H75060
 R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: H75060
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-486 <RAW>
 A:Cross-references: GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB50381.1; PID:G545889
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1391
 C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1309
 C:Keywords: oxidoreductase

 Query Match 6.5%; Score 8; DB 2; Length 486;
 Best Local Similarity 100.0%; Pred. No. 8.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

 Qy 1 MKAVLLALL 8
 Db 457 MKAVLLALL 464

 RESULT 6
 JH0447
 alpha-1A-adrenergic receptor - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
 C:Accession: JH0447
 R:Bruno, J.F.; Whittaker, J.; Song, J.; Berelowitz, M.
 Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991
 A:Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic
 A:Reference number: JH0447; MUID:92028892; PMID:1656955
 A:Accession: JH0447
 A:Molecule type: mRNA
 A:Residues: 1-501 <BRU>
 A:Cross-references: GB:M76446; NID:G177806; PIDN:AAA35496.1; PID:gl77807
 A:Experimental source: hippocampus
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:93-116/Domain: transmembrane #status predicted <TM1>
 F:128-151/Domain: transmembrane #status predicted <TM2>
 F:172-196/Domain: transmembrane #status predicted <TM3>
 F:210-233/Domain: transmembrane #status predicted <TM4>
 F:308-331/Domain: transmembrane #status predicted <TM5>
 F:339-363/Domain: transmembrane #status predicted <TM6>

 Query Match 6.5%; Score 8; DB 2; Length 501;
 Best Local Similarity 100.0%; Pred. No. 8.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

 Qy 103 AAAILALL 110
 Db 171 AAAILALL 178

 RESULT 7
 A38731
 alpha-1A adrenergic receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Apr-2000
 C:Accession: A38731; A53280
 R:Lomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Peng, T.L.
 J. Biol. Chem. 266, 6365-6369, 1991
 A:Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recept
 A:Reference number: A38731; MUID:91177889; PMID:1706716
 A:Accession: A38731
 A:Molecule type: mRNA
 A:Residues: 1-560 <LOM>
 A:Cross-references: GB:M60654; NID:G202761; PIDN:AAA63477.1; PID:G202762
 R:Perez, D.M.; Plascik, M.T.; Graham, R.M.
 Mol. Pharmacol. 40, 876-883, 1991

A;Title: Solution-phase library screening for the identification of rare clones: isolated
A;Reference number: A53280; MUID:92100054; PMID:1661838
A;Accession: A53280
A;Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A;Residues: 1-36, 'P', 38-58, 'I', 60-202, 'I', 204-305, 'R', 307-366, 'I', 368-370, 'I', 372-559 <P>
A;Experimental source: hippocampus
A;Note: sequence extracted from NCBI backbone (NCBIP:73541)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 6.5%; Score 8; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 9.3; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0

Qy 103 AAAILALL 110
|||||
Db 207 AAAILALL 214

RESULT 8
I39369
alpha-1A-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 13-Aug-1999
A;Accession: I39369; JC2331
R;Ebenschade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.; Mol. Pharmacol. 47, 977-985, 1995
A;Title: Cloning of the human alpha 1A-adrenergic receptor and inducible expression of the
A;Reference number: I39369; MUID:95265059; PMID:7746284
A;Accession: I39369
A;Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A;Residues: 1-572 <RES>
A;Cross-references: GB:D29952; NID:G914933; PIDN:BAA06222.1; PID:G914934
R;Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.; Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors and
A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2331
A:Molecule type: mRNA
A;Residues: 1-30, 'G', 32-521, 'P', 523-572 <WEI>
A;Note: the authors translated the codon CCC for residue 522 as Arg
C;Genetics:
A;Gene: GDB:ADRA1A; ADRA1R
A;Cross-references: GDB:I18749; OMIM:104219
A;Map position: 20pter-20qter
A;Introns: 37/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;89-123/Domain: transmembrane #status predicted <TM1>
F;132-162/Domain: transmembrane #status predicted <TM2>
F;172-197/Domain: transmembrane #status predicted <TM3>
F;208-235/Domain: transmembrane #status predicted <TM4>
F;254-278/Domain: transmembrane #status predicted <TM5>
F;344-374/Domain: transmembrane #status predicted <TM6>
F;380-414/Domain: transmembrane #status predicted <TM7>
F;65,82/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 8; DB 2; Length 572;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110
|||||
Db 213 AAAILALL 220

RESULT 9
T08512
trbo protein - Enterobacter aerogenes plasmid R751
C;Species: Enterobacter aerogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: T08512
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M. Plasmid 36, 95-111, 1996
A;Title: Conservation of the genetic switch between replication and transfer genes of In-
A;Reference number: Z16434; MUID:97118926; PMID:8954881
A;Accession: T08512
A;Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A;Residues: 1-88 <THO>
A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561
C;Genetics:
A;Gene: trbo
A;Genome: plasmid R751

Query Match 5.7%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 20; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 112 ALGILLW 118
|||||
Db 46 ALGILLW 52

RESULT 10
S29714
guanine-nucleotide-releasing protein mss4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
A;Accession: S29714
R;Burton, J.; Roberts, D.; Montaldi, M.; Novick, P.; de Camilli, P. Nature 361, 464-467, 1993
A;Title: A mammalian guanine-nucleotide-releasing protein enhances function of yeast sec
A;Reference number: S29714; MUID:93156814; PMID:8429887
A;Accession: S29714
A:Molecule type: mRNA
A;Residues: 1-123 <BUR>
A;Cross-references: EMBL:X70496; NID:g313871; PIDN:CAA49904.1; PID:g313872
C;Genetics:
A;Gene: mss4

Query Match 5.7%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 15 LQPGTAL 21
|||||
Db 31 LQPGTAL 37

RESULT 11
I52427
guanine-nucleotide-releasing protein Mss4 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
A;Accession: I52427
R;Yu, H.; Schreiber, S.L. Biochemistry 34, 9103-9110, 1995
A;Title: Cloning, Zn2+ binding, and structural characterization of the guanine nucleotide
A;Reference number: I52427; MUID:95345082; PMID:7619808
A;Accession: I52427
A;Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A;Residues: 1-123 <RES>
A;Cross-references: GB:S78873; NID:g1037135; PIDN:AAB34955.1; PID:g1037136
C;Genetics:
A;Gene: GDB:MSS4
A;Cross-references: GDB:683578

Query Match 5.7%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 15 LQPGTAL 21

Db 31 LQGTAL 37
|||||

RESULT 12
F82716
hypothetical protein XF1150 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: F82716
R/anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: F82716
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-123 <SIM>
A/Cross-references: GB:AE003950; GB:AE003849; NID:G9106104; PIDN:AAF83960.1; GSPDB:GN00148
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laioir Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Nunes, L.R.; Oliveira, M.A.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak N.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z M.; Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF1150

Query Match 5.7%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LPALGGL 116
|||||

Db 98 LPALGGL 104
|||||

RESULT 13
T22693
hypothetical protein F55B11.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T22693
R/Ainscough, R.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z19601
A/Accession: T22693
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-145 <WIL>
A/Cross-references: EMBL:Z83318; PIDN:CAB05900.1; GSPDB:GN00022; CESP:F55B11.4
A/Experimental source: clone F55B11
C/Genetics:
A/Gene: CESP:F55B11.4
A/Map position: 4
A/Introns: 15/1; 54/1; 114/1

Query Match 5.7%; Score 7; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 TVISKGC 66
|||||

Db 53 TVISKGC 59
|||||

RESULT 14
E87507
hypothetical protein CC2086 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: E87507
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Esmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: E87507
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-150 <STO>
A/Cross-references: GB:AE005673; NID:gl3423567; PIDN:AAK34057.1; GSPDB:GN00148
C/Genetics:
A/Gene: CC2086

Query Match 5.7%; Score 7; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 LLPALGL 115
|||||

Db 86 LLPALGL 92
|||||

RESULT 15
T48784
hypothetical protein 13E11.320 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
C/Accession: T48784
R/Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000
A/Reference number: Z24541
A/Accession: T48784
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-166 <SCH>
A/Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:13E11.320
A/Experimental source: cosmid contig 13E11; strain 74
C/Genetics:
A/Gene: NCSP:13E11.320
A/Map position: 2
C/Superfamily: Neurospora crassa hypothetical protein 13E11.320

Query Match 5.7%; Score 7; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 PALGLLL 117
|||||

Db 96 PALGLLL 102
|||||

Search completed: August 18, 2003, 19:57:29
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:45:04 ; Search time 23 Seconds
(without alignments)
251.491 Million cell updates/sec

Title: US-09-934-586A-2

Perfect score: 123
Sequence: 1 MKAVLLALLMAGLALQFGTA.....AAILALLPALGLLWGPQGL 123

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	75.6	123	1	PSCA_HUMAN
2	8	6.5	123	1	PSCA_MOUSE
3	8	6.5	176	1	VG12_BPMU
4	8	6.5	267	1	GLNR_STRCO
5	8	6.5	561	1	AIAD_RAT
6	8	6.5	562	1	AIAD_MOUSE
7	8	6.5	572	1	AIAD_HUMAN
8	8	6.5	576	1	AIAD_RABIT
9	7	5.7	123	1	MSS4_HUMAN
10	7	5.7	123	1	MSS4_MOUSE
11	7	5.7	123	1	MSS4_RAT
12	7	5.7	193	1	LEPT_BACSU
13	7	5.7	206	1	FGF4_HUMAN
14	7	5.7	206	1	SOMA_PROAN
15	7	5.7	213	1	ER21_CAEEL
16	7	5.7	252	1	GPH_ECO57
17	7	5.7	252	1	GPH_ECOLI
18	7	5.7	252	1	GPH_SALTI
19	7	5.7	252	1	GPH_SALTY
20	7	5.7	253	1	GPH_KLEAE
21	7	5.7	287	1	YXKE_BACSU
22	7	5.7	345	1	Y141_MYCTU
23	7	5.7	406	1	DAC_STRSO
24	7	5.7	438	1	GLNA_RHOCA
25	7	5.7	454	1	TRIA_MOUSE
26	7	5.7	461	1	TRIA_RAT
27	7	5.7	467	1	GLNA_AZOV1
28	7	5.7	467	1	GLNA_RHOSH
29	7	5.7	467	1	TM11_MOUSE
30	7	5.7	468	1	GLNA_AZOB1
31	7	5.7	468	1	GLNA_ECOLI
32	7	5.7	468	1	GLNA_SALTY
33	7	5.7	468	1	TM11_HUMAN

34	7	5.7	469	1	GLN1_STRRP	P77958 streptomyce
35	7	5.7	472	1	GLNA_HABIN	P43794 haemophilus
36	7	5.7	472	1	GLNA_NEIGO	P25821 neisseria g
37	7	5.7	472	1	GLNA_PASMU	O9clp2 pasteurella
38	7	5.7	492	1	CP51_SORBI	P93846 sorghum bic
39	7	5.7	494	1	EXOT_RHIME	P33699 rhizobium m
40	7	5.7	508	1	GSH1_MEDTR	O2znx6 medicago tr
41	7	5.7	514	1	GSH1_BRAJU	O23736 brassica ju
42	7	5.7	522	1	GSH1_ATH	P46309 arabidopsis
43	7	5.7	523	1	GSH1_LYCES	O22493 lycopersico
44	7	5.7	531	1	PMO1_CANPA	Q951a2 canis famil
45	7	5.7	544	1	FUS1_YEAST	Q12211 saccharomyc

ALIGNMENTS

RESULT 1	
PSCA_HUMAN	
ID PSCA_HUMAN	STANDARD; PRT; 123 AA.
AC O43653;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Prostate stem cell antigen precursor.	
GN PSCA.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Prostatic carcinoma;	
RX MEDLINE=98132663; PubMed=9465086;	
RA Reiter R.E., Gu Z., Watabe T., Thomas G., Szigeti K., Davis E.,	
RA Wahl M., Nisitani S., Yamashiro J., le Beau M.M., Loda M., Witte O.N.;	
RT "Prostate stem cell antigen: a cell surface marker overexpressed in	
RT prostate cancer.";	
RL Proc. Natl. Acad. Sci. U.S.A. 95:1735-1740(1998).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Urothelial;	
RA Bahrenberg G., Joost H.G.;	
RT "Serial analysis of the gene expression of a highly differentiated	
RT urothelial tumor.";	
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.	
RN [3]	
RP TISSUE SPECIFICITY.	
RC MEDLINE=20180504; PubMed=10713670;	
RA Gu Z., Thomas G., Yamashiro J., Shintaku I.P., Dorey F., Raitano A.,	
RA Witte O.N., Said J.W., Loda M., Reiter R.E.;	
RT "Prostate stem cell antigen (PSCA) expression increases with high	
RT gleason score, advanced stage and bone metastasis in prostate	
RT cancer.";	
RL Oncogene 19:1288-1296(2000).	
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.	
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE (BASAL, SECRETORY	
CC (NEUROENDOCRINE EPITHELIUM CELLS), ALSO FOUND IN BLADDER	
CC (TRANSITIONAL EPITHELIUM), PLACENTA (TROPHOBLASTS), STOMACH	
CC (NEUROENDOCRINE CELLS), COLON (NEUROENDOCRINE CELLS) AND KIDNEY	
CC (COLLECTING DUCTS). OVEREXPRESSED IN PROSTATE CANCERS AND	
CC EXPRESSION IS CORRELATED WITH TUMOR STAGE, GRADE AND ANDROGEN-	
CC INDEPENDENCE. HIGHLY EXPRESSED IN PROSTATE CANCER BONE METASTASES.	
CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.	
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CC -----	

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DR EMBL; AF043498; AAC39607.1; -.
DR EMBL; AJ297436; CAB97347.1; -.
DR Genbank; HGNC:9500; PSCA.
DR MIM; 602470; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0008222; F:tumor antigen; TAS.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR_LY6_1.
DR PRODOM; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6 UPAR; 1.
DR Signal; Antigen; Glycoprotein; Membrane; GPI-anchor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 95 PROSTATE STEM CELL ANTIGEN.
FT PROPEP 96 123 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 21 95 UPAR/LY6.
FT DISULFID 23 48 BY SIMILARITY.
FT DISULFID 26 35 BY SIMILARITY.
FT DISULFID 41 66 BY SIMILARITY.
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 87 92 BY SIMILARITY.
FT CARBOHYD 90 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 95 95 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 123 AA; 12912 MW; 3FC1271742D657FA CRC64;

Query Match 75.6%; Score 93; DB 1; Length 123;
Best Local Similarity 100.0%; Pred.No.1.9e-82;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALPGTALLCYSCKAQVNEQCLQVENCQTOLGEOCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALPGTALLCYSCKAQVNEQCLQVENCQTOLGEOCWTARIRAVGLLT 60

Qy 61 VISKGSCLNCVDDSDQYVGVKKNTCCDIDLCLN 93
Db 61 VISKGSCLNCVDDSDQYVGVKKNTCCDIDLCLN 93

RESULT 2
PSCA_MOUSE STANDARD; PRT; 123 AA.
AC PS7036;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prostate stem cell antigen precursor.
GN PSCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE-Petal and Kidney;
CC MEDLINE=98132661; PubMed=9465086;
CC Reiter R.E., Gu Z., Wakabe T., Thomas G., Szigeti K., Davis E.,
CC Wahl M., Nistatani S., Yamashiro J., le Beau M.M., Losa M., Witte O.N.;
CC "Prostate stem cell antigen: a cell surface marker overexpressed in
CC prostate cancer";
CC Proc. Natl. Acad. Sci. U.S.A. 95:1735-1740(1998).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PROSTATE. ALSO
CC FOUND IN SPLEEN, LIVER, LUNG, PROSTATE, KIDNEY AND TESTIS.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC HSP; P13987; 1ERG.
CC MGB; MGI:1919623; PscA.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR_LY6_1.
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DR PRODOM; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6 UPAR; 1.
DR Antigen; Glycoprotein; Membrane; GPI-anchor; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 95 PROSTATE STEM CELL ANTIGEN.
FT PROPEP 96 123 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 21 95 UPAR/LY6.
FT DISULFID 23 48 BY SIMILARITY.
FT DISULFID 26 35 BY SIMILARITY.
FT DISULFID 41 66 BY SIMILARITY.
FT DISULFID 70 86 BY SIMILARITY.
FT DISULFID 87 92 BY SIMILARITY.
FT CARBOHYD 90 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 95 95 GPI-ANCHOR (BY SIMILARITY).
SQ SEQUENCE 123 AA; 13443 MW; CDA8566F37307ECC CRC64;

Query Match 6.5%; Score 8; DB 1; Length 123;
Best Local Similarity 100.0%; Pred.No.1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 TVISKGCS 67
Db 60 TVISKGCS 67

RESULT 3
VG12_BPUM STANDARD; PRT; 176 AA.
AC Q38488; Q9TIX6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein gp12 (Protein E13).
GN 12 OR E13.
OS Bacteriophage Mu.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC Mu-like viruses.
OX NCBI_TaxID=10677;
CC [1]
CC SEQUENCE FROM N.A.
CC Pries H., Brauer B., Schmidt C., Kamp D.;
CC "Sequence of the left end of Mu.";
CC (In) Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.);
CC Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press,
CC New York (1987).
CC [2]
CC SEQUENCE FROM N.A.
CC Morgan G., Hatfull G., Hendrix R.;
CC "Genome of bacteriophage Mu and comparison with the Haemophilus
CC influenzae Mu-like prophage Flumu.";
CC Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M64097; AAA32400.1; -.
CC EMBL; AF083977; AAF01089.1; -.
CC Hypothetical protein.
FT CONFLICT 46 46 S -> C (IN REF. 1).
SQ SEQUENCE 176 AA; 19895 MW; 44E199AAAFBC4BESD CRC64;

Query Match 6.5%; Score 8; DB 1; Length 176;
Best Local Similarity 100.0%; Pred.No.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 ALLPALGL 115
```

|||||
115 ALLPALGL 122

RESULT 4

GLNR_STRCO STANDARD; PRT; 267 AA.
ID GLNR_STRCO STANDARD; PRT; 267 AA.
AC Q05943;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transcriptional regulatory protein glnr.
GN GLNR OR SCO4159 OR SCD84.26C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=93345814; PubMed=7688332;
RA Wray L.V. Jr., Fisher S.H.;
RT "The Streptomyces coelicolor glnr gene encodes a protein similar to
other bacterial response regulators.";
RL Gene 130:145-150(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser K., Lark L., Murphy L., Oliver K., O'Neil S.,
Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).

CC -1- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE GLNA GENE.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; L03213; AAA02838.1; --
DR EMBL; AL339119; CAB88492.1; --
DR PIR; JN0831; JN0831.
DR HSP; P08402; 1QOI.
DR InterPro; IPR001867; Trans reg C.
DR Pfam; PF00486; trans reg C; 1.
DR ProDom; PD000329; Trans reg C; 1.
KW Sensory transduction; Phosphorylation; Transcription regulation;
KW DNA-binding; Activator; Complete proteome.
FT MOD_RES 50 50 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE. 267 AA; 28887 MW; 54069CDB07C1BFBI CRC64;

Query Match 6.5%; Score 8; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LPALGLLL 1175

Db 18 LPALGLLL 25

RESULT 5

ALAD_RAT STANDARD; PRT; 561 AA.
ID ALAD_RAT STANDARD; PRT; 561 AA.
AC P23944;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A
adrenergic receptor) (RA42).
GN ADRA1D OR ADRA1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=91177889; PubMed=1706716;
RA Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A.,
Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.;
RT "Molecular cloning and expression of the cDNA for the alpha 1A-
adrenergic receptor. The gene for which is located on human
chromosome 5.";
RL J. Biol. Chem. 266:6365-6369(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=95114877; PubMed=7815325;
RX Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
Worman N.P., Campbell S., Fidock M.D., Furness L.M.,
Parry-Smith D.J., Peter B., Bailey D.S.;
RT "Cloning and pharmacological characterization of human alpha-1
adrenergic receptors: sequence corrections and direct comparison with
other species homologues.";
RL J. Pharmacol. Exp. Ther. 272:134-142(1995).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: VAS DEFERENS, HIPPOCAMPUS, CEREBRAL CORTEX,
AORTA, BRAIN STEM, HEART AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; M0654; AAA63477.1; --
DR EMBL; L31771; AAB59704.1; --
DR PIR; A38731; A38731.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1_1_000PSN.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 90 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 91 115 1 (POTENTIAL).
FT DOMAIN 116 127 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 128 153 2 (POTENTIAL).
FT DOMAIN 154 163 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 164 186 3 (POTENTIAL).
FT DOMAIN 187 207 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 208 232 4 (POTENTIAL).
FT DOMAIN 233 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 269 5 (POTENTIAL).
FT DOMAIN 270 342 6 (POTENTIAL).
FT TRANSMEM 343 367 7 (POTENTIAL).
FT DOMAIN 368 374 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 375 399 7 (POTENTIAL).
FT DOMAIN 400 561 CYTOPLASMIC (POTENTIAL).

RT "The alpha 1-adrenergic receptor that mediates smooth muscle
RT contraction in human prostate has the pharmacological properties of
RT the cloned human alpha 1c subtype."
RL Mol. Pharmacol. 45:703-708(1994).

RL [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95114877; PubMed=7815325;
RA Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
RA Worman N.P., Campbell S., Fiddock M.D., Furness L.M.,
RA Parry-Smith D.J., Peter B., Bailey D.S.;
RA "Cloning and pharmacological characterization of human alpha-1
RT adrenergic receptors: sequence corrections and direct comparison with
RT other species homologues."
RL J. Pharmacol. Exp. Ther. 272:134-142(1995).

RL [4]
RN SEQUENCE FROM N.A.
RP MEDLINE=94296402; PubMed=8024574;
RX Weinberg D.H., Irivadi P., Tan C.P., Mitra S., Perkins-Barrow A.,
RA Borkowski D., Strader C.D., Bayne M.;
RA "Cloning, expression and characterization of human alpha adrenergic
RT receptors alpha 1a, alpha 1b and alpha 1c."
RL Biochem. Biophys. Res. Commun. 201:1296-1304(1994).

RL [5]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [6]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [7]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [8]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [9]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [10]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

RL [11]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta, and Prostate;
RX MEDLINE=95265059; PubMed=7746284;
RA Esbenhade T.A., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
RA Minneman K.P., Murphy T.J.;
RA "Cloning of the human alpha 1d-adrenergic receptor and inducible
RT expression of three human subtypes in SK-N-MC cells."
RL Mol. Pharmacol. 47:977-985(1995).

FT DOMAIN 160 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 192 3 (POTENTIAL).
FT DOMAIN 173 213 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 214 238 4 (POTENTIAL).
FT DOMAIN 239 251 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 252 275 5 (POTENTIAL).
FT DOMAIN 276 348 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 349 373 6 (POTENTIAL).
FT DOMAIN 374 380 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 381 405 7 (POTENTIAL).
FT DOMAIN 406 572 CYTOPLASMIC (POTENTIAL).
FT LIPID 419 419 PALMITATE (POTENTIAL).
FT DOMAIN 422 428 POLY-ARG.
FT CONFLICT 1 83 MTRDLLSVFEGPRDPDSSAGGSGAGGSGAGGAGPSEG
FT PAVGGVPGAGGGGAVGAGSGEDNRSSAGGPGSAGAGGD
FT VNG -> MAALRSVMAGYLSWRTPTSTSTVMVQLRM
FT EAVQHS (IN REF. 1).
FT S -> G (IN REF. 4).
FT CONFLICT 31 31 KPSSAFREWLGLGFRPTTQLRKAVSLSHKIRAGGAQR
FT CONFLICT 489 572 AEACARQSEVAVSLGVPHEVAGATCQAYELADYNLR
FT ETDI -> SHPAPSAGCGWGRSGDPRSPCAPKSPACRTR
FT SPGARSARQORAPSAORWRLCP (IN REF. 1).
FT CONFLICT 522 522 R -> P (IN REF. 4).
FT SEQUENCE 572 AA; 60462 MW; EBEI134CF20A4988 CRC64;
Query Match 6.5%; Score 8; DB 1; Length 572;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 AAAILALL 110
Db 213 AAAILALL 220
RESULT 8
ALAD RABIT STANDARD; PRT; 576 AA.
ID AC 002666; Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor).
GN ADRA1D.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97182161; PubMed=9030207;
RA Suzuki F., Miyamoto S., Takita M., Oshita M., Watanabe Y.,
RA Kakizuka A., Narumiya S., Taniguchi T., Muramatsu I.;
RT "Cloning, functional expression and tissue distribution of rabbit
RL alpha 1d-adrenoceptor."
CC Biochim. Biophys. Acta 1323:6-11(1997).
CC -1- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
CC THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U64032; AAB53098.1; -;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR

DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
 FT MULTIGENE FAMILY; Phosphorylation; Lipoprotein; Palmitate.
 FT DOMAIN 1 101
 FT TRANSMEM 102 126
 FT DOMAIN 127 138
 FT TRANSMEM 129 164
 FT DOMAIN 165 174
 FT TRANSMEM 175 197
 FT DOMAIN 198 218
 FT TRANSMEM 219 243
 FT DOMAIN 244 256
 FT TRANSMEM 257 280
 FT DOMAIN 281 353
 FT TRANSMEM 354 378
 FT DOMAIN 379 385
 FT TRANSMEM 386 410
 FT DOMAIN 411 576
 FT CARBOHYD 70 70
 FT CARBOHYD 87 87
 FT LIPID 424 424
 FT DOMAIN 54 59
 FT DOMAIN 78 84
 FT DOMAIN 427 433
 SQ SEQUENCE 576 AA; 60266 MW; 21EDF1025D0144CE CRC64;

Query Match 6.5%; Score 8; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110
 Db 218 AAAILALL 225

RESULT 9
 ID MSS4 HUMAN STANDARD; PRT; 123 AA.
 AC P47224; Q92992;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Guanine nucleotide exchange factor MSS4 (Rab interacting factor).
 GN RABIF OR RASGRF3 OR MSS4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Yu H., Schreiber S.L.;
 RT "Cloning, Zn²⁺ binding, and structural characterization of the
 RL guanine nucleotide exchange factor human Mss4.";
 RL Biochemistry 34:9103-9110(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=98110574; PubMed=9441742;
 RA Mueller-Pillasch F., Zimmerhackl F., Lacher U., Schultz N.,
 RA Haneister H., Varga G., Friess H., Buechler M., Adler G., Gress T.M.;
 RT "Cloning of novel transcripts of the human guanine nucleotide-exchange
 RT factor Mss4: in situ chromosomal mapping and expression in pancreatic
 RT cancer.";
 RL Genomics 46:389-396(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaracne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95379975; PubMed=7651540;
 RA Yu H., Schreiber S.L.;
 RT "Structure of guanine-nucleotide-exchange factor human Mss4 and
 RT identification of its rab-interacting surface.";
 RL Nature 376:788-791(1995).
 CC -!- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
 CC MEMBERS OF THE SCB4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
 CC FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
 CC THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
 CC TRANSPORT.
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
 CC
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 CC
 CC EMBL; S78873; AAB34955.1; -;
 CC EMBL; U74324; AAB18264.1; -;
 CC EMBL; BC018488; AAB18488.1; -;
 CC PIR; 152427; I52427.
 CC PDB; 1FMG; 04-OCT-00.
 CC Genew; HGNC:9797; RABIF.
 CC MIN; 603417; -;
 CC GO; GO:0005085; F:guanyl-nucleotide exchange factor activity; TAS.
 CC GO; GO:0006944; P:membrane fusion; TAS.
 CC GO; GO:0006899; P:non-selective vesicle transport; TAS.
 CC Pfam; PF04421; Mss4; 1.
 CC Guanine-nucleotide releasing factor; Protein transport; Zinc;
 KW 3D-structure.
 KW METAL 23
 FT METAL 23
 FT METAL 26
 FT METAL 94
 FT METAL 97
 FT CONFLICT 5
 FT STRAND 11
 FT STRAND 11
 FT STRAND 16
 FT STRAND 21
 FT TURN 24
 FT TURN 28
 FT TURN 33
 FT TURN 37
 FT STRAND 43
 FT TURN 48
 FT TURN 56
 FT STRAND 63
 FT STRAND 68
 FT HELIX 74
 FT STRAND 83
 FT STRAND 89

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FT TURN 95 96
FT STRAND 103 106
FT TURN 110 111
FT STRAND 113 116
FT TURN 118 119
FT STRAND 121 123
SQ SEQUENCE 123 AA; 13839 MW; 78E98395FAE10257 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LQPGTAL 21
DB 31 LQPGTAL 37

RESULT 10
MSS4_MOUSE STANDARD; PRT; 123 AA.
AC Q91X36;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide exchange factor MSS4 (Rab interacting factor);
OS RABIF.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
MEMBERS OF THE SEC4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
TRANSPORT (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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CC -----
DR EMBL: BC011166; AAH11166.1;
DR MGD; MGI:2138605; AW549708.
DR Pfam; PF04421; Mss4; 1.
KW Guanine-nucleotide releasing factor; Protein transport; Zinc.

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FT METAL 23 23 ZINC (BY SIMILARITY).
FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
SQ SEQUENCE 123 AA; 13915 MW; 73FAEBC0DBE8B02 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LQPGTAL 21
DB 31 LQPGTAL 37

RESULT 11
MSS4_RAT STANDARD; PRT; 123 AA.
AC Q08326;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide exchange factor MSS4 (RAB interacting factor).
OS RABIF OR MSS4.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93156814; PubMed=8429887;
RA Burton J., Roberts D., Montaldi M., Novick P., de Camilli P.;
RT "A mammalian guanine-nucleotide-releasing protein enhances function
of yeast secretory protein Sec4";
RL Nature 361:464-467(1993).
CC -1- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
MEMBERS OF THE SEC4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
TRANSPORT.
CC -1- TISSUE SPECIFICITY: Ubiquitous.
CC -1- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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CC -----
DR EMBL: X70496; CAA49904.1;
DR PIR; S29714; S29714.
DR PDB; 1HXR; 04-APR-01.
DR Pfam; PF04421; Mss4; 1.
KW Guanine-nucleotide releasing factor; Protein transport; Zinc;
3D-structure.
FT METAL 23 23 ZINC (BY SIMILARITY).
FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT STRAND 11 11
FT TURN 11 11
FT STRAND 13 13
FT STRAND 16 16
FT STRAND 21 21
FT TURN 24 24
FT STRAND 29 29
FT TURN 33 33
FT STRAND 37 37
FT STRAND 43 43
FT STRAND 49 49
FT HELIX 51 54

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FT TURN 56 57
FT STRAND 62 65
FT STRAND 68 71
FT HELIX 74 76
FT STRAND 81 82
FT STRAND 86 86
FT TURN 87 - 88
FT STRAND 89 93
FT TURN 95 97
FT STRAND 99 100
FT STRAND 103 106
FT TURN 107 108
FT TURN 110 111
FT STRAND 113 116
FT HELIX 117 119
FT STRAND 120 123
SQ SEQUENCE 123 AA; 13928 MW; ACB7D07E2735811C CRC64;

Query Match 5.7%; Score 7; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LQPGTAL 21
Db 31 LQPGTAL 37
|||||

RESULT 12
LEPT BACSU STANDARD; PRT; 193 AA.
AC P71013;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Signal peptidase I T (EC 3.4.21.89) (Spase I) (Leader peptidase I).
GN SIPT.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Tjalma H., Bolhuis A., Bron S., Venema G., van Dijk J.M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RX MEDLINE=98044033; PubMed=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Enrian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

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RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapollak S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegg T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yamamoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256 (1997).
CC -1- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
CC secreted proteins precursor.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26.
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-----
CC EMBL; U45883; AAB07348.1; -.
CC EMBL; AF012285; AAC24916.1; -.
CC EMBL; Z99111; CAB13314.1; -.
CC PIR; G69707; G69707.
CC HSP; P00803; IB12.
CC MEROPS; S26.004; -.
CC Subtilisin; Bcl1977; sipt.
CC InterPro; IPR000508; SigPrase.
CC InterPro; IPR000223; SigPrase_S26A.
CC Pfam; PF00461; Peptidase_S26; 1.
CC PRINTS; PR00727; LEADERPTASE.
CC PROSITE; PS00501; SPASE_1; 1.
CC PROSITE; PS00760; SPASE_2; 1.
CC PROSITE; PS00761; SPASE_3; 1.
CC Transmembrane; Hydrolase; Protease; Complete proteome.
KW DOMAIN 1 25 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 26 42 POTENTIAL.
FT DOMAIN 43 193 EXTRACELLULAR (POTENTIAL).
FT ACT_SITE 51 93 BY SIMILARITY.
FT ACT_SITE 93 93 BY SIMILARITY.
SQ SEQUENCE 193 AA; 21854 MW; 6746B4C38037F3C9 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AVLLALL 9
Db 30 AVLLALL 36
|||||

RESULT 13
FGF4 HUMAN
ID_FGF4_HUMAN STANDARD; PRT; 206 AA.
AC P08620;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF-
DE 4).
GN FGF4 OR HST OR HSTF1 OR KS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041096; PubMed=2959959;
RA Yoshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
RA Terada M., Sugimura T.;
RT "Genomic sequence of hst, a transforming gene encoding a protein
RT homologous to fibroblast growth factors and the int-2-encoded
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87204251; PubMed=2953031;
RA Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
RA Sugimura T.;
RT "cDNA sequence of human transforming gene hst and identification of
RT the coding sequence required for transforming activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87301716; PubMed=2957062;
RA Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
RA Basiglio C.;
RT "An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes
RT a growth factor that is a member of the FGF family.";
RL Cell 50:729-737(1987).
CC -1- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOMACH TUMOR
CC (HST) AND FROM KARPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC
CC ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02986; AAB59555.1; -
DR EMBL; M17446; AAB59473.1; -
DR PIR; A28417; TVRHHS.
DR PDB; 1IJT; 15-AUG-01.
DR Genew; HGNC:3682; FGF4.
DR MIM; 164980; -
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0008083; P:growth factor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007048; P:oncogenesis; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR002348; 3I1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; I1I_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Proto-oncogene; Growth_factor; Mitogen; Signal; 3D-structure.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 206 FIBROBLAST GROWTH FACTOR-4.
SQ SEQUENCE 206 AA; 22047 MW; C7FD54A0272A1569 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AVLLALL 9
Db 14 AVLLALL 20

RESULT 14
SOMA_PROAN

```

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ID AC 073848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN GH.
OS Protopterus annectens (African lungfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Dipnoi; Lepidosireniformes; Protoptera; Protopterus.
OX NCBI_TaxID=7888;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pituitary;
RA May D., Alrubatan J., Patel S., Doris R.M., Rand-Weaver M.;
RT "Studies on the GH/SL gene family: cloning of African lungfish
RT (Protopterus annectens) growth hormone and somatolactin and toad (Bufo
RT marinus) growth hormone.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth hormone plays an important role in growth control
CC and is involved in the regulation of several anabolic processes.
CC Implicated as an osmoregulatory substance important for seawater
CC adaptation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF062745; AAC16496.1; -
DR HSP; P01241; IHUW.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PROSITE; PS00266; SOMATOTROPIN_1; FALSE_NEG.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hormone; Pituitary; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 206 SOMATOTROPIN.
FT DISULFID 75 179 BY SIMILARITY.
FT DISULFID 196 204 BY SIMILARITY.
SQ SEQUENCE 206 AA; 23407 MW; 9ED9D1E3BC307B57 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LLALLMA 11
Db 10 LLALLMA 16

RESULT 15
ER21 CAEEL
ID ER21 CAEEL STANDARD; PRT; 213 AA.
AC Q09473;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ER lumen protein retaining receptor C28H8.4.
GN C28H8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoida;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N., Waterston R.;

```

Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for the retention of luminal endoplasmic
CC reticulum proteins. Determines the specificity of the luminal ER
CC protein retention system. Also required for normal vesicular
CC traffic through the Golgi (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE ERD2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20861; AAA62292.1; -;
DR PIR; H88469; H88469.
DR WormPep; C28H8.4; CE01826.
DR InterPro; IPR000133; ERret_receptor.
DR Pfam; PF00810; ER_lumen_recept; 1.
DR PRINTS; PR00860; ERLUMENR.
DR PRODOM; PD005774; ERret_receptor; 1.
DR PROSITE; PS00951; ER_LUMEN_RECEPTOR_1; 1.
DR PROSITE; PS00952; ER_LUMEN_RECEPTOR_2; 1.
KW Hypothetical protein; Endoplasmic reticulum; Transmembrane;
KW Protein transport; Receptor.
FT DOMAIN 1 2 LUMENAL (POTENTIAL).
FT TRANSMEM 3 21 POTENTIAL.
FT DOMAIN 22 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 53 POTENTIAL.
FT DOMAIN 54 61 LUMENAL (POTENTIAL).
FT TRANSMEM 62 80 POTENTIAL.
FT DOMAIN 81 96 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 97 110 POTENTIAL.
FT DOMAIN 111 117 LUMENAL (POTENTIAL).
FT TRANSMEM 118 137 POTENTIAL.
FT DOMAIN 138 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 168 POTENTIAL.
FT DOMAIN 169 178 LUMENAL (POTENTIAL).
FT TRANSMEM 179 199 POTENTIAL.
FT DOMAIN 200 213 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 213 AA; 24742 MW; 2F6400E38D8D8CF4 CRC64;

Query Match 5.7%; Score 7; DB 1; Length 213;
Best Local Similarity 100.0%; Pred.No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 104 AAILALL 110
Db 102 AAILALL 108
|||||

Search completed: August 18, 2003, 19:54:58
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:51:35 ; Search time 97 Seconds
(without alignments)
327.221 Million cell updates/sec

Title: US-09-934-586A-2
Perfect score: 123
Sequence: 1 MKAVLLALLMAGLALQPGTA.....AAILALLPALGLLLMGPGQL 123

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL 23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	9	7.3	300	16 Q9KY91	Q9ky91 streptomyc
2	8	6.5	123	11 Q9D700	Q9d700 mus musculu
3	8	6.5	140	11 Q9WU26	Q9wu26 cavia porce
4	8	6.5	167	10 Q8S7G7	Q8s7g7 oryza sativ
5	8	6.5	249	16 Q88YV4	Q88yv4 rhizobium l
6	8	6.5	279	16 Q8FV23	Q8fv23 bruceella su
7	8	6.5	284	5 Q21073	Q21073 caenorhabdi
8	8	6.5	299	16 Q8YE18	Q8ye18 bruceella me
9	8	6.5	370	4 Q9H1N4	Q9h1n4 homo sapien
10	8	6.5	486	17 Q9UVN1	Q9uvn1 pyrococcus
11	8	6.5	559	11 Q9QW71	Q9qw71 tatusu sp.
12	8	6.5	571	6 Q3TWN9	Q3twn9 sus scrofa
13	8	6.5	602	8 Q956R5	Q956r5 iguana igua
14	7	5.7	62	16 Q9KIM3	Q9kim3 streptomyc
15	7	5.7	75	2 Q8GQV9	Q8gqv9 thiobacillu
16	7	5.7	75	2 Q8GQV5	Q8gqv5 thiobacillu

17	7	5.7	75	2 Q8GQY2	Q8gqv2 thiobacillu
18	7	5.7	88	2 P71190	P71190 escherichia
19	7	5.7	88	9 Q9AZ53	Q9az53 lactococcus
20	7	5.7	88	9 Q38613	Q38613 lactococcus
21	7	5.7	88	9 Q37968	Q37968 bacterioph
22	7	5.7	89	2 Q8RSI3	Q8rsi3 uncultured
23	7	5.7	91	2 Q06656	Q06656 streptomyc
24	7	5.7	96	11 Q8BLK0	Q8blk0 mus musculu
25	7	5.7	98	2 Q93BC6	Q93bc6 salmonella
26	7	5.7	101	13 Q8JHF0	Q8jhf0 brachydanio
27	7	5.7	104	2 Q93BF4	Q93bf4 salmonella
28	7	5.7	106	2 Q93BD5	Q93bd5 salmonella
29	7	5.7	108	2 Q93BD2	Q93bd2 salmonella
30	7	5.7	109	2 Q93BC1	Q93bc1 salmonella
31	7	5.7	110	2 Q93BH2	Q93bh2 salmonella
32	7	5.7	111	2 Q93BE4	Q93be4 salmonella
33	7	5.7	114	2 Q93BD4	Q93bd4 salmonella
34	7	5.7	114	11 Q8BGI9	Q8bgi9 mus musculu
35	7	5.7	115	2 Q93BF2	Q93bf2 salmonella
36	7	5.7	116	2 Q93BE3	Q93be3 salmonella
37	7	5.7	117	2 Q93B84	Q93b84 salmonella
38	7	5.7	117	2 Q93BH1	Q93bh1 salmonella
39	7	5.7	118	2 Q932V6	Q932v6 salmonella
40	7	5.7	118	2 Q93BE7	Q93be7 salmonella
41	7	5.7	118	2 Q93BD6	Q93bd6 salmonella
42	7	5.7	120	2 Q93BC0	Q93bc0 salmonella
43	7	5.7	120	2 Q93BF1	Q93bf1 salmonella
44	7	5.7	121	2 Q93BE9	Q93be9 salmonella
45	7	5.7	121	2 Q933F2	Q933f2 salmonella

ALIGNMENTS

RESULT 1

Q9KY91 ID Q9KY91 PRELIMINARY; PRT; 300 AA.
AC Q9KY91; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative integral membrane protein.
GN SCO5011 OR SCK15.13.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,
RA Huang C.-H., Kisser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939122; CAB92604.1; -.
KW Complete proteome.
SQ SEQUENCE 300 AA; 32763 MW; 3BDA1EA5DD2BB7F4 CRC64;

Query Match 7.3%; Score 9; DB 16; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AVLLALLMA 11
|||||

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Db          7 AVLLALLMA 15
RESULT 2
Q9D7U0      PRELIMINARY;      PRT;      123 AA.
AC Q9D7U0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 2210408B04RIK protein (Prostate stem cell antigen).
GN PSCA OR 2210408B04RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Harsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21371909; PubMed=11479226;
RA Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
RT "Murine six-transmembrane epithelial antigen of the prostate, prostate
RT stem cell antigen, and prostate-specific membrane antigen: prostate-
RT specific cell-surface antigens highly expressed in prostate cancer of
RT transgenic adenocarcinoma mouse prostate mice.";
RL Cancer Res. 61:5857-5860(2001).
DR EMBL; AK008851; BAB25929.1; -
DR EMBL; AF319173; AAK84073.1; -
DR HSSP; P13987; IERG.
DR MGP; MGI:1919623; PscA.
DR InterPro; IPR003632; Ly6-6 CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR_Ly6_1.
DR ProDom; PD003128; Ly6-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; 1.
SQ SEQUENCE 123 AA; 13477 MW; 67A8566F3D30797A CRC64;

Query Match 6.5%; Score 8; DB 11; Length 123;
Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 60 TVISKGCS 67
Db 60 TVISKGCS 67

RESULT 3
Q9WU26
Q9WU26      PRELIMINARY;      PRT;      140 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-1D adrenergic receptor (Fragment).
GN ADRA1D.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20079491; PubMed=10611446;
RA Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M.,
RA Gonzalez-Espinosa D., Garcia-Sainz J.A.;
RT "Inverse alpha(1A) and alpha(1D) adrenoceptor mRNA expression during
RT isolation of hepatocytes.";
RL Eur. J. Pharmacol. 384:231-237(1999).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF108017; AAD22541.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRRHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15185 MW; 59AF5E8D5E1DDEF6 CRC64;

Query Match 6.5%; Score 8; DB 11; Length 140;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 AAAILALL 110
Db 80 AAAILALL 87

RESULT 4
Q8S7G7      PRELIMINARY;      PRT;      167 AA.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 18.6 kDa protein.
GN OSJNB0048D20.6.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Taiten T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNB0048D20 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084766; AAL82515.1; -
DR Gramene; Q8S7G7; -
KW Hypothetical protein.
SQ SEQUENCE 167 AA; 18582 MW; 11C5F3EA7341BEF0 CRC64;

Query Match 6.5%; Score 8; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 8.9;

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 PAAAILAL 109

Db 134 PAAAILAL 141

RESULT 5

ID Q98IY4 PRELIMINARY; PRT; 249 AA.

AC Q98IY4;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein ml12193.

GN ML12193.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MAFF303099;

RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,

RA Takeuchi C., Yanada M., Tabata S.,

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Mesorhizobium loti";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP002999; BAB49382.1; -

DR InterPro; IPR002781; DUF81.

DR Pfam; PF01925; DUF81; 1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 249 AA; 25285 MW; 5B70922CEA5703C CRC64;

Query Match

Best Local Similarity 6.5%; Score 8; DB 16; Length 249;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 106 ILALLPAL 113

Db 203 ILALLPAL 210²

RESULT 6

ID Q8FY23

AC Q8FY23 PRELIMINARY; PRT; 279 AA.

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Conserved hypothetical protein.

GN BR2067.

OS Brucella suis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29461;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1330 / Biovar 1;

RX MEDLINE=22247741; PubMed=12271122;

RA Paulsen I.F., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,

RA Daugherty S.C., Deboy B.T., Durkin A.S., Kolonay J.F., Madupu R.,

RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

RT "The Brucella suis genome reveals fundamental similarities between

RT animal and plant pathogens and symbionts.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

DR EMBL; AE014494; AAN30957.1; -

DR TIGR; BR2067; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 279 AA; 30481 MW; 452110EFCDD36FA5 CRC64;

Query Match

Best Local Similarity 6.5%; Score 8; DB 16; Length 279;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110

Db 262 AAAILALL 269

RESULT 7

ID Q21073

AC Q21073 PRELIMINARY; PRT; 284 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE K01A6.4 protein.

GN K01A6.4.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Cottage A.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology.";

RL Science 282:2012-2018(1998).

DR EMBL; Z68750; CAA92963.1; -

DR WormPep; K01A6.4; CE06037.

SQ SEQUENCE 284 AA; 27053 MW; C5A748D8E72DE82D CRC64;

Query Match

Best Local Similarity 6.5%; Score 8; DB 5; Length 284;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KAVLLALL 9

Db 4 KAVLLALL 11

RESULT 8

ID Q8YE18

AC Q8YE18 PRELIMINARY; PRT; 299 AA.

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE ATP/GTP-binding protein.

GN BMEI2060.

OS Brucella melitensis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29459;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=16M / ATCC 23456 / Biotype 1;

RX MEDLINE=20020109; PubMed=11756688;

RA Delvecchio V.G., Kapural V., Redkar R.J., Patra G., Mujer C., Los T.,

RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goitman E.,

RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyrpides N., Overbeek R.;

RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009638; AAL53241.1; -.
 DR InterPro; IPR005177; DUF299.
 DR Pfam; PF03618; DUF299; 1.
 KW Complete proteome.
 SQ SEQUENCE 299 AA; 32663 MW; 9312097DIC525123 CRC64;

Query Match 6.5%; Score 8; DB 16; Length 299;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110³
 Db 282 AAAILALL 289
 |||||

RESULT 9
 Q9HIN4 PRELIMINARY; PRT; 370 AA.
 AC Q9HIN4
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE BA137P16.1 (Adrenergic, alpha-1D-, receptor (alpha 1D-adrenoreceptor))
 DE (Fragment).
 GN ADRA1D.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramsay H.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AL357040; CAC17424.1; -.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP Fl_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 FT NON_TER 370 370
 SQ SEQUENCE 370 AA; 37915 MW; . A2D5AFBB2BD7751B CRC64;

Query Match 6.5%; Score 8; DB 4; Length 370;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110³
 Db 213 AAAILALL 220
 |||||

RESULT 10
 Q9UYN1 PRELIMINARY; PRT; 486 AA.
 AC Q9UYN1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hydrogenase-4 component D (EC 1.-.-.-).
 GN PAB1391.
 OS Pyrococcus abyssi.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=29292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;

RA Heilig R.;
 RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
 RT structure and evolution";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
 CC CHAINS.
 DR EMBL; AJ248287; CAB50381.1; -.
 DR InterPro; IPR003916; NADHub_oxred5.
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; oxidored_q1; 1.
 DR PRINTS; PR01434; NADHHDGNASE5.
 KW NAD; Oxidoreductase; Complete proteome.
 SQ SEQUENCE 486 AA; 53669 MW; 8C996E4F6A0C5CBA CRC64;

Query Match 6.5%; Score 8; DB 17; Length 486;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAVLLAL 8
 Db 457 MKAVLLAL 464
 |||||

RESULT 11
 Q9QW71 PRELIMINARY; PRT; 559 AA.
 ID Q9QW71
 AC Q9QW71; 2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Alpha 1-adrenergic receptor subtype alpha 1D, alpha 1D-AR.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92100054; PubMed=1661818;
 RA Perez D.M., Piascik M.T., Graham R.M.;
 RT "Solution-phase library screening for the identification of rare
 RT clones: isolation of an alpha 1b-adrenergic receptor cDNA";
 RL Mol. Pharmacol. 40:876-883(1991).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECP Fl_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 559 AA; 59739 MW; 37CD9BD69D3A47D CRC64;

Query Match 6.5%; Score 8; DB 11; Length 559;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAAILALL 110
 Db 207 AAAILALL 214
 |||||

RESULT 12
 Q9TTM9 PRELIMINARY; PRT; 571 AA.
 ID Q9TTM9
 AC Q9TTM9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Alpha-1D adrenergic receptor.
 GN ALPHA-1D.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

```

OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RA Uhlen S., Waith A.;
RT "Characterization of the pig alpha-1D adrenergic receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ250492; CAB59347.1; -.
DR EMBL; AJ250493; CAB59347.1; JOINED.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 571 AA; 60698 MW; BACFFB5C903972B1 CRC64;

Query Match 6.5%; Score 8; DB 6; Length 571;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 103 AAALLALL 110
Db 212 AAALLALL 219
|||||

RESULT 13
Q956R5 PRELIMINARY; PRT; 602 AA.
AC Q956R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 5.
GN NADH5.
OS Iguana iguana (Common iguana).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21190842; PubMed=11297180;
RA Janke A., Erpenbeck D., Nilsson M., Arnason U.;
RT "The mitochondrial genomes of the iguana (Iguana iguana) and the
RT caiman (Caiman crocodylus): Implications for amniote phylogeny.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:623-631(2001).
RN [2]
RN SEQUENCE FROM N.A.
RA Janke A.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278511; CAC37093.1; -.
DR InterPro; IPR003916; NADHhub_oxred5.
DR InterPro; IPR001750; Oxidored_q1.
DR InterPro; IPR001516; Oxidored_q1_N.
DR Pfam; PF00361; oxidored_q1; 1.
DR Pfam; PF00662; oxidored_q1_N; 1.
DR PRINTS; PR01434; NADHDKGNASES.
KW NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SQ SEQUENCE 602 AA; 66177 MW; 820FAP8A2D4CD92B CRC64;

Query Match 6.5%; Score 8; DB 8; Length 602;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 LPALGGLL 117
Db 211 LPALGGLL 218
|||||

RESULT 14
Q9KIM3 PRELIMINARY; PRT; 62 AA.
AC Q9KIM3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE F3a (Hypothetical 6.3 kDa protein).
DE F23a OR SCO4189 OR 2SCD46.03C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=A3(2); AND M145;
RA Kormanec J., Sevcikova B., Homerova D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [5]
RN SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AF230488; AAF82057.1; -.
DR EMBL; AL939119; CAC04025.1; -.
KW Complete proteome.
SQ SEQUENCE 62 AA; 6276 MW; F3D69CEE87375643 CRC64;

Query Match 5.7%; Score 7; DB 16; Length 62;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AVLLALL 9
Db 50 AVLLALL 56
|||||

RESULT 15
Q8GQY9 PRELIMINARY; PRT; 75 AA.
AC Q8GQY9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sub-unit III of an aad-type cytochrome oxidase (fragment).

```

GN COXC.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23270;
RA Sasaki K., Ida C., Matsumoto N., Ando A., Saiki H., Ohmura N.;
RT "Respiratory isozyme, two types of rusticyanin of Acidithiobacillus
ferrooxidans.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094630; BAC22699.1; -.
FT NON TER 1
SQ SEQUENCE 75 AA; 8530 MW; D94B010FF2FC014D CRC64;

Query Match 5.7%; Score 7; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AAILALL 110
| | | | |
Db 25 AAILALL 31

Search completed: August 18, 2003, 19:56:43
Job time : 99 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:32:04 ; Search time 23 Seconds
(without alignments)
251.491 Million cell updates/sec

Title: US-09-934-586a-2

Perfect score: 646

Sequence: 1 MKAVLLALLMAGLAPGTA.....AAILALLPALGLLWPGQL 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	99.8	123	1	PSCA_HUMAN
2	388	60.1	123	1	PSCA_MOUSE
3	172.5	26.7	126	1	LY6E_CHICK
4	158.5	24.5	131	1	LY6E_HUMAN
5	144	22.3	130	1	LY6E_MOUSE
6	126	19.5	127	1	LY6D_MOUSE
7	121.5	18.8	103	1	SLUR_HUMAN
8	115.5	17.9	116	1	LYNX_MOUSE
9	114.5	17.7	140	1	LY6H_HUMAN
10	111.5	17.3	126	1	LG6C_MOUSE
11	111	17.2	139	1	LY6H_MOUSE
12	101	15.6	125	1	LG6C_HUMAN
13	99.5	15.4	110	1	SLUR_MOUSE
14	96.5	14.9	79	1	NXS6_PSETE
15	96.5	14.9	126	1	CD59_PAPSP
16	95	14.7	128	1	LY6D_HUMAN
17	95	14.7	222	1	UPAS_MOUSE
18	95	14.7	327	1	UPAR_MOUSE
19	94.5	14.6	126	1	CD59_RAT
20	94	14.6	511	1	AVRB_XENLA
21	93	14.4	83	1	CK7P_NAJAT
22	92.5	14.3	128	1	CD59_HUMAN
23	92.5	14.3	328	1	UPAR_RAT
24	91	14.1	83	1	CKH_NAJNA
25	91	14.1	512	1	AVRB_HUMAN
26	90	13.9	536	1	AVRB_MOUSE
27	89.5	13.9	79	1	NXS7_PSETE
28	89.5	13.9	285	1	ASPX_PAPHA
29	89	13.8	83	1	CK7A_NAJAT
30	89	13.8	220	1	UPAS_RAT
31	88.5	13.7	265	1	ASPX_HUMAN
32	87	13.5	158	1	GML_HUMAN
33	86.5	13.4	99	1	SVS7_MOUSE

34	86.5	13.4	128	1	CD59_AOTTR
35	86	13.3	134	1	LY6I_MOUSE
36	85.5	13.2	79	1	NXS2_PSETE
37	85.5	13.2	99	1	RSPI_RAT
38	85	13.2	86	1	TSYL_DENAN
39	85	13.2	86	1	TXM2_DENAN
40	84.5	13.1	79	1	NXS3_PSETE
41	84.5	13.1	89	1	NXH6_BUNMU
42	84.5	13.1	512	1	AVRB_BOVIN
43	84	13.0	128	1	CD59_CERA
44	83.5	12.9	79	1	NXS1_PSETE
45	83.5	12.9	89	1	NXH3_BUNMU

PS1447	aotus trivi
Q9wu67	mus musculus
Q9w7k1	pseudonaja
Q9qxn2	rattus norv
PI7696	dendroaspis
PI8328	dendroaspis
Q9w7k0	pseudonaja
O12963	bungarus mu
Q95126	bos taurus
Q28216	cercopithec
Q9w7k2	pseudonaja
Q3y9j0	bungarus mu

ALIGNMENTS

RESULT 1

ID	PSCA_HUMAN	STANDARD;	PRT;	123 AA.
AC	O43653;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Prostate stem cell antigen precursor.			
GN	PSCA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostatic carcinoma;			
RX	MEDLINE=98132663; Pubmed=9465086;			
RA	Reiter R.E., Gu Z., Watabe T., Thomas G., Szigeti K., Davis E.,			
RA	Wahl M., Nisitani S., Yamashiro J., le Beau M.M., Loda M., Witte O.N.;			
RT	"Prostate stem cell antigen: a cell surface marker overexpressed in prostate cancer.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:1735-1740(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Urothelial;			
RA	Bahrenberg G., Joost H.G.;			
RT	"Serial analysis of the gene expression of a highly differentiated urothelial tumor.";			
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	TISSUE SPECIFICITY.			
RX	MEDLINE=20180504; PubMed=10713670;			
RA	Gu Z., Thomas G., Yamashiro J., Shintaku I.P., Dorey F., Raitano A.,			
RA	Witte O.N., Said J.W., Loda M., Reiter R.E.;			
RT	"Prostate stem cell antigen (PSCA) expression increases with high gleason score, advanced stage and bone metastasis in prostate cancer.";			
RL	Oncogene 19:1288-1296(2000).			
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.			
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE (BASAL, SECRETORY AND NEUROENDOCRINE EPITHELIUM CELLS). ALSO FOUND IN BLADDER (TRANSITIONAL EPITHELIUM), PLACENTA (TROPHOBLASTS), STOMACH (NEUROENDOCRINE CELLS), COLON (NEUROENDOCRINE CELLS) AND KIDNEY (COLLECTING DUCTS). OVEREXPRESSED IN PROSTATE CANCERS AND EXPRESSION IS CORRELATED WITH TUMOR STAGE, GRADE AND ANDROGEN-INDEPENDENCE. HIGHLY EXPRESSED IN PROSTATE CANCER BONE METASTASES.			
CC	-1- SIMILARITY: Contains 1 UPAR/Ly6 domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			


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CC ENBL; L34554; AAA49063.1; --
DR InterPro; IPR003632; LY-6 CD59.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR LY6; 1.
DR ProDom; PD003128; LY-6-CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6 UPAR; FALSE NEG.
KW Signal; Antigen; Multigene family; Membrane; GPI-anchor.
FT SIGNAL 1 20
FT CHAIN 21 298
FT PROPEP 299 126
FT DOMAIN 21 98
FT DISULFID 23 48
FT DISULFID 26 35
FT DISULFID 41 69
FT DISULFID 73 89
FT DISULFID 90 95
FT CARBOHYD 96 96
FT LIPID 98 98
SQ SEQUENCE 126 AA; 13011 MW; EB5C9B6674C73B8 CRC64;

Query Match 26.7%; Score 172.5; DB 1; Length 126;
Best Local Similarity 35.5%; Pred. No. 9.9e-11;
Matches 43; Conservative 21; Mismatches 48; Indels 9; Gaps 3;

QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCNTOLGEOCWTARIRAVGL-- 58
DB 1 MKAFPLFAVLAVLCVERAHTLIFCSQDASNNACLTPVKAENEHCVTYV-GVGIGG 59

QY 59 --LTVISKGSCLNCVDDSDQYVYVKKNTCCDIDLKXSAHALQPAALALLPALGLL 116
DB 60 KSGQISIKGSGPCPSAGINLGIAAASVYCCDSFLCNSGSSVKASYAVL----ALGIL 115

QY 117 L 117
DB 116 V 116

RESULT 4
LY6E HUMAN STANDARD; PRT; 131 AA.
AC Q16553;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lymphocyte antigen Ly-6E precursor (Retinoic acid-induced gene E protein) (RIG-E) (Thymic shared antigen-1) (TSA-1) (Stem cell antigen 2) (SCA-2).
DE LY6E OR RIGE OR TSA1 OR SCA2 OR 9804.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Promyelocytic leukemia;
MEDLINE=96234063; PubMed=8650192;
Mao M., Yu M., Tong J.-H., Ye J., Zhu J., Huang Q.-H., Fu G., Yu L., Zhao S.-Y., Waxman S., Lanotte M., Wang Z.-Y., Tan J.-Z., Chan S.-J., Chen Z.;
"RIG-E, a human homolog of the murine Ly-6 family, is induced by retinoic acid during the differentiation of acute promyelocytic leukemia cell.";
Proc. Natl. Acad. Sci. U.S.A. 93:5910-5914 (1996).
[2]
SEQUENCE FROM N.A.
TISSUE=Brain, and Breast;
MEDLINE=96338150; PubMed=8757598;
Capone M.C., Gorman D.M., Ching E.P., Zlotnik A.;
"Identification through bioinformatics of cDNAs encoding human thymic shared Ag-1/stem cell Ag-2: A new member of the human Ly-6 family.";
J. Immunol. 157:969-973 (1996).

```

```

[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Monocytes;
RX MEDLINE=98211698; PubMed=9551972;
Shan X., Bourdeau A., Rhoton A., Wells D.E., Cohen E.H., Landgraf B.E., Palfree R.G.E.;
"Characterization and mapping to human chromosome 8q24.3 of Ly-6-related gene 9804 encoding an apparent homologue of mouse TSA-1.";
J. Immunol. 160:197-208 (1998).
RL -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, PREDOMINANTLY IN LIVER, KIDNEY, OVARY, SPLEEN AND PERIPHERAL BLOOD LEUKOCYTES.
CC -1- INDUCTION: BY RETINOIC ACID; IN PROMYELOCYTIC LEUKEMIA NB4 AND IN MVELOBLAST HL-60 CELL LINES. ACTIVATED BY INF-ALPHA IN MONOCYTIC CELL LINE U-937 AND IN PERIPHERAL BLOOD MONOCYTE CELLS.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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CC ENBL; U42376; AAC50519.1; --
DR ENBL; U56145; AAC50616.1; --
DR ENBL; U66711; AAB07513.1; --
DR ENBL; Z68179; CAA92321.1; --
DR Genew; HGNC:6727; LY6E.
DR MIM; 601384; --
DR GO; GO:0005887; C-integral to plasma membrane; TAS.
DR GO; GO:0007166; P-cell surface receptor linked signal transdu. . . ; TAS.
DR InterPro; IPR003632; LY-6 CD59.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR LY6; 1.
DR ProDom; PD003128; LY-6 CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6 UPAR; FALSE NEG.
KW Signal; Antigen; Multigene family; Membrane; GPI-anchor.
FT SIGNAL 1 20
FT CHAIN 21 101
FT PROPEP 102 131
FT DOMAIN 21 101
FT DISULFID 23 48
FT DISULFID 26 35
FT DISULFID 41 71
FT DISULFID 75 92
FT DISULFID 93 98
FT CARBOHYD 99 99
FT LIPID 101 101
SQ SEQUENCE 131 AA; 13507 MW; 0F6D1157741AFC98 CRC64;

Query Match 24.5%; Score 158.5; DB 1; Length 131;
Best Local Similarity 35.3%; Pred. No. 2.7e-09;
Matches 47; Conservative 18; Mismatches 53; Indels 15; Gaps 5;

QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCNTOLGEOCWTARIRA-VGLL 59
DB 1 MKIFLPVLLAALLGVERRASSLMCFCLNQKSNLYCLKPTICSDQDNYCVTVSASAGIGNL 60
QY 60 TV----ISKGCSLNC-VDDSDQYVYVKKNTCCDIDLKXSGAH-----ALOPRAAIL 107
DB 61 VTFGHSLSKTCSPACPIPEGVNVGVASMGISCCQFLCNFSAADGGLRASVTLLGAGLLL 120
QY 108 ALLPALGLLLWGP 120
DB 121 SLLPA--LLRFGP 131

RESULT 5

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LY6E MOUSE
ID LY6E_MOUSE STANDARD; PRT; 130 AA.
AC Q64253; Q61128;
DT 15-JUN-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lymphocyte antigen Ly-6E precursor (Thymic shared antigen-1) (TSA-1)
DE (stem cell antigen 2)
GN LY6E OR LY67 OR SCA-2 OR TSA-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94081342; PubMed=8258699;
RA Macneil I., Kennedy J., Godfrey D.I., Jenkins N.A., Masciantonio M.,
RA Mineo C., Gilbert D.J., Copeland N.G., Boyd R.L., Zlotnik A.;
RT "Isolation of a cDNA encoding thymic shared antigen-1. A new member
of the Ly6 family with a possible role in T cell development.";
RL J. Immunol. 151:6913-6923(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Thymus;
RC MEDLINE=94261572; PubMed=8202484;
RA Classon B.J., Coverdale L.;
RT "Mouse stem cell antigen Sca-2 is a member of the Ly-6 family of cell
surface proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5296-5300(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SvJ;
RC MEDLINE=96270003; PubMed=8662090;
RA Classon B.J., Coverdale L.;
RT "Genomic organization and expression of mouse thymic shared antigen-1
(TSA-1): evidence for a processed pseudogene";
RL Immunogenetics 44:222-226(1996).
CC -1- FUNCTION: INVOLVED IN T-CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.

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DR EMBL; U09192; AAB03366.1; ALT INIT.
DR EMBL; U04268; ABA19121.1; ALT_INIT.
DR EMBL; U47737; AAB17698.1; -;
DR MGI; 106651; Ly6e.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR_Ly6_1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; FALSE NEG.
DR Signal; Antigen; Multigene family; Membrane; GPI-anchor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 1 20 LYMPHOCYTE ANTIGEN LY-6E.
FT PROPEP 103 130 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 21 101 UPAR/Ly6.
FT DISULFID 23 48 BY SIMILARITY.
FT DISULFID 26 35 BY SIMILARITY.
FT DISULFID 41 70 BY SIMILARITY.
FT DISULFID 74 92 BY SIMILARITY.
FT DISULFID 93 98 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC...) (POTENTIAL).
FT LIPID 102 102 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 130 AA; 13800 MW; 0D1C2505F61DEB2 CRC64;

Query Match 22.3%; Score 144; DB 1; Length 130;
Best Local Similarity 30.8%; Pred. No. 7.9e-08;
Matches 40; Conservative 20; Mismatches 60; Indels 10; Gaps 3;
QY 1 MKAVLALLMAGLALPGTALLCYSCAKVSNEDCLQVENCCTOLGQCWTARIRA-----V 56
DB 1 MRVFLVLLAALMGVQVHSLMFCSTQDKNNINCLWPVSCQEKDHYCITLSAAGFGNV.60
QY 57 GLLTVTSKGCINCVDDSDYVYVKKNIT--CCDTLCKNKS-----GAHALQPAALALL 110
DB 61 NLGYTLKNGCSPICPSNVNVLNGLVASVNSYCCQSFNFAAGLGLRASIPLLGLLL 120
QY 111 PALGLLLWGP 120
DB 121 SLALLQLSP 130
RESULT 6
LY6E_MOUSE
ID LY6E_MOUSE STANDARD; PRT; 127 AA.
AC P35459;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphocyte antigen Ly-6D precursor (Thymocyte B cell antigen) (Thb).
GN LY6D OR THB OR LY61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Thymocytes;
RC MEDLINE=93017863; PubMed=1401899;
RA Gumley T.P., McKenzie I.F., Kozak C.A., Sandrin M.S.;
RT "Isolation and characterization of cDNA clones for the mouse
thymocyte B cell antigen (Thb).";
RL J. Immunol. 149:2615-2618(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Leukocyte;
RC MEDLINE=95369850; PubMed=7642235;
RA Gumley T.P., McKenzie I.F., Sandrin M.S.;
RT "Sequence and structure of the mouse Thb gene.";
RL Immunogenetics 42:221-224(1995).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: THYMOCYTES AND B CELLS.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.

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DR EMBL; X63782; CAA45317.1; -;
DR EMBL; L40419; AAA79249.1; ALT_INIT.
DR PIR; A46528; A46528.
DR MGI; 96881; Ly6d.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR_Ly6_1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; 1.
DR Signal; Antigen; Multigene family; Membrane; GPI-anchor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 1 98 LYMPHOCYTE ANTIGEN LY-6D.
FT PROPEP 99 127 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 21 108 UPAR/Ly6.
FT DISULFID 23 45 BY SIMILARITY.

FT DISULFID 26 32 BY SIMILARITY.
 FT DISULFID 38 63 BY SIMILARITY.
 FT DISULFID 67 86 BY SIMILARITY.
 FT DISULFID 87 92 BY SIMILARITY.
 FT LIPID 98 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 127 AA; 13395 MW; 0AF039B77D105917 CRC64;

Query Match 19.5%; Score 126; DB 1; Length 127;
 Best Local Similarity 31.8%; Pred. No. 5.1e-06;
 Matches 42; Conservative 19; Mismatches 51; Indels 20; Gaps 7;

Qy 1 MKAVILLALLMAGLALQPTALLCYSCAKQVSNEDCLQVNTQGEQCWTARIRAVGLL- 59
 Db 1 MKTALLVLLVAVTSPAWALRHVC---TNSANCKNPQVCPNSFYFCKT--VTSVEPLN 55
 Qy 60 -TVISKCSLNCVDD-SQDYV--GKNITCCDIDLGN-----XSGAHALQPA-----AA 105
 Db 56 GNLVRKCANCTSDYSQQHVSSESVTQCCQDLCNRLVSAAPGHALLSSVTGLAT 115
 Qy 106 ILALLPALGLLL 117
 Db 116 SLSLLTVMALCL 127

RESULT 7
 SLURP_HUMAN STANDARD; PRT; 103 AA.
 AC P55080; Q92483;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secreted Ly-6/uPAR related protein 1 precursor (SLURP-1) (ARS
 DE component B) (ARS(Component B)-81/S) (Anti-neoplastic urinary protein)
 DE (ANUP).
 GN SLURP1 OR ARS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Mastrangeli R.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE OF 22-36.
 RP TISSUE=Granulocyte;
 RX MEDLINE=96351837; PubMed=8742060;
 RA Ridge R.J., Sloane N.H.;
 RT "Partial N-terminal amino acid sequence of the anti-neoplastic
 RT urinary protein (ANUP) and the anti-tumour effect of the N-terminal
 RT nonapeptide of the unique cytokine present in human granulocytes.";
 RL Cytokine 8:1-5(1996).
 RN [3]
 RP PARTIAL SEQUENCE.
 RP MEDLINE=99226809; PubMed=10211827;
 RA Andermann K., Wattler F., Wattler S., Heine G., Meyer M.,
 RA Forssmann W.-G., Nehls M.;
 RT "Structural and phylogenetic characterization of human SLURP-1, the
 RT first secreted mammalian member of the Ly-6/uPAR protein
 RT superfamily.";
 RL Protein Sci. 8:810-819(1999).
 RN [4]
 RP DISEASE.
 RX MEDLINE=21181711; PubMed=11285253;
 RA Fischer J., Boudjar B., Heilig R., Huber M., Lefevre C., Jobard F.,
 RA Macari F., Bakija-Konsuo A., Ait-Belkacem F., Weissbach J.,
 RA Lathrop M., Hohl D., Prud'homme J.-F.;
 RT "Mutations in the gene encoding SLURP-1 in Mal de Meleda.";
 RL Hum. Mol. Genet. 10:875-880(2001).
 CC -1- FUNCTION: Has an antitumor activity.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: GRANULOCYTES. EXPRESSED IN SKIN.
 CC -1- DISEASE: Defects in SLURP1 are a cause of Mal de Meleda (MDM), a
 CC rare autosomal recessive skin disorder, characterized by
 CC transgressive palmo-plantar keratoderma (ppk), keratotic skin
 CC lesions, perioral erythema, brachydactyly and nail abnormalities.
 CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC -1- CAUTION: IT IS NOT CERTAIN THAT ARS AND ANUP ARE IDENTICAL
 CC PROTEINS.
 CC -----
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 CC -----
 DR EMBL; X99977; CAA68237.1; -;
 DR PIR; A59031; A59031.
 DR MIM; 606119; -;
 DR MIM; 248300; -;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005125; F:Cytokine activity; NAS.
 DR InterPro; IPR003632; Ly-6_CD59.
 DR InterPro; IPR001526; Ly6_UPAR.
 DR Pfam; PF00021; UPAR_Ly6; 1.
 DR ProDom; PD003128; Ly-6_CD59; 1.
 DR SMART; SM0134; LU; 1.
 DR PROSITE; PS00983; LY6_UPAR; FALSE_NEG.
 DR Cytokine; Signal.
 KW SIGNAL 1 21
 FT CHAIN 22 103 SECRETED LY-6/UPAR RELATED PROTEIN 1.
 FT DOMAIN 24 73 UPAR/LY6.
 FT DISULFID 25 50 POTENTIAL.
 FT DISULFID 28 37 POTENTIAL.
 FT DISULFID 43 73 POTENTIAL.
 FT DISULFID 77 93 POTENTIAL.
 FT DISULFID 94 99 POTENTIAL.
 FT CONFLICT 22 22 A -> Q (IN REF. 2).
 FT CONFLICT 36 36 S -> A (IN REF. 2).
 SQ SEQUENCE 103 AA; 11186 MW; 07AAF6BCA8031282 CRC64;

Query Match 18.8%; Score 121.5; DB 1; Length 103;
 Best Local Similarity 29.7%; Pred. No. 1.2e-05;
 Matches 27; Conservative 13; Mismatches 46; Indels 5; Gaps 1;

Qy 8 LLMAGLALQPTALLCYSCAKQVSNEDCLQVNTQGEQCWTARIRA-----VGLLTVI 62
 Db 10 LLVAASMGCGEALKCYTCCKEPMTSASCRITTRCKPEDTACMTTLTVTEAEYFPNQSPV 69
 Qy 63 SKGSLNCVDDSDQYVYVKKNICTCDIDLGN 93
 Db 70 TRSCSSCVATDPDSIGAHLIFCCFRDLGN 100

RESULT 8
 LYNX_MOUSE STANDARD; PRT; 116 AA.
 AC Q9WVC2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ly-6/neurotoxin-like protein 1 precursor (GC26).
 GN LYNX1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Cerebellum;
 RX MEDLINE=99328647; PubMed=10402197;
 RA Miwa J.M., Ibanez-Tallon I., Crabtree G.W., Sanchez R., Sali A.,

RA Role L.W., Heintz N.;
 RT "Lynx1, an endogenous toxin-like modulator of nicotinic acetylcholine
 RL receptors in the mammalian CNS."; Neuron 23:105-114(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Miwa J.M., Fletcher C.F., Copeland N.G., Jenkins N.A., Heintz N.;
 RT "Genetic mapping and characterization of Lynx1: a new member of the
 RL Ly6/neurotoxin superfamily."; J. Neurosci. 19:105-114(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Aeshburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=21904935; PubMed=11906696;
 RA Ibanez-Tallon I., Miwa J.M., Wang H.L., Adams N.C., Crabtree G.W.,
 RA Sine S.M., Heintz N.;
 RT "Novel modulation of neuronal nicotinic acetylcholine receptors by
 RL association with the endogenous prototoxin lynx1"; Neuron 33:893-903(2002).
 CC -!- FUNCTION: Seems to modulate nicotinic acetylcholine receptors.
 CC Promotes the largest of three current amplitudes elicited by ACh
 CC through alpha(4)beta(2) nAChRs and that LYNX1 enhances
 CC desensitization.
 CC -!- SUBUNIT: Binds directly to nAChRs.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor

CC (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in brain. Expressed in neurons in
 CC multiple brain structures.
 CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC -----
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 CC -----
 CC EMBL; AF141377; AAD38939.1; -
 CC EMBL; AF169202; AAF16899.1; -
 CC EMBL; AK013827; BAB29006.1; -
 CC EMBL; BC037541; AAH37541.1; -
 CC DR MGD; MG11345180; Lynx1.
 CC DR InterPro; IPR003632; Ly-6_CDS9.
 CC DR InterPro; IPR001526; Ly6 UPAR.
 CC Pfam; PF00021; UPAR_LY6; 1.
 CC ProDom; PD003128; Ly-6_CDS9; 1.
 CC DR SMART; SM00134; LU; 1; CDS9; 1.
 CC DR GPI-anchor; Membrane; Signal.
 CC KW SIGNAL 1 20 POTENTIAL.
 CC FT CHAIN 21 93 LY-6/NEUROTOXIN-LIKE PROTEIN 1.
 CC FT PROPEP 94 116 REMOVED IN MATURE FORM (POTENTIAL).
 CC FT DOMAIN 21 107 UPAR/LY6.
 CC FT DISULFID 23 46 BY SIMILARITY.
 CC FT DISULFID 26 33 BY SIMILARITY.
 CC FT DISULFID 39 64 BY SIMILARITY.
 CC FT DISULFID 68 85 BY SIMILARITY.
 CC FT DISULFID 86 91 BY SIMILARITY.
 CC FT LIPID 93 93 GPI-ANCHOR (POTENTIAL).
 CC SQ SEQUENCE 116 AA; 12835 MW; DAF42FCIA34DE85 CRC64;
 CC -----
 CC Query Match 17.9%; Score 115.5; DB 1; Length 116;
 CC Best Local Similarity 27.7%; Pred. No. 5.5e-05;
 CC Matches 33; Conservative 15; Mismatches 64; Indels 7; Gaps 3;
 CC -----
 CC Oy 1 MKAVILLALLMAGLALQPTALLCYSCAQSVDCLQVNCVTCGECWTRARIVAGLLT 60
 CC Db 1 MTHLLTTFVLVLMGLPVAQALECHVC--AYNGDNCFKMPCPNATYCTTTRVTFPYRM 58
 CC Oy 61 VISKGSCLNCDVSDQYVCKKNIT-CCDTDLCKXGHAHALQPAALAILLALGLLLW 118
 CC Db 59 KVRKSCVPSCFETVYDGYKHSASATSCQYLCNGAGF----ATPVTIALVPALLATFW 113
 CC -----
 CC RESULT 9
 CC LY6H HUMAN
 CC ID LY6H_HUMAN .STANDARD; PRT; 140 AA.
 CC AC 094772;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CC DE Lymphocyte antigen Ly-6H precursor.
 CC GN Ly6H.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Fetal brain;
 CC RX MEDLINE=99017973; PubMed=9799603;
 CC RA Horie M., Okutomi K., Taniguchi Y., Ohbuchi Y., Suzuki M.,
 CC RA Takahashi E.-I.;
 CC RT "Isolation and characterization of a new member of the human Ly6 gene
 CC family (LY6H)."; Genomics 53:365-368(1998).
 CC RL [2]
 CC RP SEQUENCE FROM N.A.

```

Db      65 KHSVNMKCASSC--DFVKRHFFSDYLMGFINSGLKVDVDCCEKOLCNGAAGAGHSFWA 122
Qy      105 AIALLPALG-LILL-GP 120
Db      123 LAGGLLLSLGFPALLWAGP 140

RESULT 10
LG6C_MOUSE
ID LG6C_MOUSE STANDARD; PRT; 126 AA.
AC Q9Z1Q4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
DE G24).
DE GN LY6G6C OR NG24.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Rowen L., Madan A., Qin S., Shaffer T., Ratcliffe A., Abbasi N.,
RA Dickhoff R., James R., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class III
RT region.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.
CC -----
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CC -----
DR EMBL; AF109905; AAC84157.1; -.
DR MGD; MGI:2148930; Ly6g6c.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 126 LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS G6C
FT PROTEIN.
FT SEQUENCE 126 AA; 14066 MW; 6D8611F9E83B97ED CRC64;

Query Match 17.3%; Score 111.5; DB 1; Length 126;
Best Local Similarity 31.8%; Pred. No. 0.00015;
Matches 41; Conservative 19; Mismatches 52; Indels 17; Gaps 7;

Qy 1 MKAVILALLMAGIALQFGTALICYSKQAQVSNEDCLQVENC-TQLGEQCWTARAVGLL 59
Db 1 MKHLLLTLSALLYCVMSADTRCHSC-YKVPVLGCVDRQSCRLEPGHKLTINV-VILGKM 58
Qy 60 TVTSKCSLNC-----VDSQDYVYG-KNITCCDTDLNCXSCAHALQPAAILAL 109
Db 59 WFFS-----NLRCGFPPEPCREVFNETHKLGLNYNTCCDKDN CN-SPAPRPTPALALISL 114
Qy 110 LPALGLLLW 118
Db 115 TSLAGLGLW 123

RESULT 11
LY6H_MOUSE
ID LY6H_MOUSE STANDARD; PRT; 139 AA.
AC Q9WUC3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

```
DE Lymphocyte antigen Ly-6H precursor.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=94432011; PubMed=10501842;
RA Apostolopoulos J., Chisholm L.J., Sandrin M.S.;
RT "Identification of mouse Ly6H and its expression in normal tissue.";
RL Immunogenetics 49:987-990(1999).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
similarity).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN, ALSO FOUND IN
CC LOWER LEVELS IN EYE AND REPRODUCTIVE TISSUES.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING EMBRYONIC
CC DEVELOPMENT.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
-----
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-----
DR EMBL; AF127091; AAD28600.1; ALT_INIT.
DR MGD; MGI:1346030; Ly6h.
DR InterPro; IPR001526; Ly6 UPAR.
DR Pfam; PF00021; UPAR LY6; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6 UPAR; FALSE NEG.
KW Signal, Antigen; Multigene family; Membrane; GPI-anchor.
FT SIGNAL 1 25
FT CHAIN 26 110
FT PROPEP 111 139
FT DOMAIN 26 113
FT DISULFID 26 51
FT DISULFID 31 39
FT DISULFID 44 72
FT DISULFID 76 103
FT DISULFID 104 109
FT CARBOHYD 35 35
FT LIPID 110 110
FT SEQUENCE 139 AA; 14669 MW; FDEEC13591EF219C CRC64;
-----
Query Match 17.2%; Score 111; DB 1; Length 139;
Best Local Similarity 29.7%; Pred. No. 0.00019;
Matches 41; Conservative 16; Mismatches 59; Indels 22; Gaps 7;
-----
QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENC-TQLGECQWTARIRAVGLLT 60
DB 6 MKSLGLALLLCPSPAGHLWCQDC--TLANSHCAKQKQOPTTVCASVRIIDPSSSR 63
-----
QY 61 ---VTSKGSCLNCVDD-----SDYYVG-----KKNITCCDTLCLNKGSAHALQAPAA 104
DB 64 KDHVSNKWCASC--DFVKRHFFSDYLMGFNSGLKVDVDCCKEKLNGASVAGRSPPA 121
-----
QY 105 AIALLLPALG-LLWL-GP 120
DB 122 LAGGLLSLGPALLWAGP 139
-----
RESULT 12
LG6C_HUMAN
ID LG6C_HUMAN STANDARD; PRT; 125 AA.
AC O95867;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
-----
28-FEB-2003 (Rel. 41, Last annotation update)
DE Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
NG24).
GN LY6G6C OR NG24 OR C6ORF24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22074936; PubMed=12079290;
RA Mallory M., Campbell R.D., Aguado B.;
RT "Transcriptional analysis of a novel cluster of LY-6 family members in
the human and mouse major histocompatibility complex: five genes with
many splice forms.";
RL Genomics 80:113-123(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Lasky S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
region.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shiina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.
-----
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-----
DR EMBL; AJ315533; CAC85539.1; -.
DR EMBL; AF129756; AAD18076.1; -.
DR EMBL; AP000504; BAB63379.1; -.
DR Genew; HGNC:13936; LY6G6C.
DR SMART; SM00134; LU; 1.
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 125
FT SEQUENCE 125 AA; 13821 MW; 9ED7549894C71311 CRC64;
-----
Query Match 15.6%; Score 101; DB 1; Length 125;
Best Local Similarity 25.5%; Pred. No. 0.0017;
Matches 38; Conservative 23; Mismatches 50; Indels 18; Gaps 9;
-----
QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENC-TQLGECQWTARIRAVGLL 59
DB 1 MKALML-LTSLVLLCWVSADIRCHSC-YKVPVLCVDRQSCRLEPGQQLTTH-AYLGKM 57
-----
QY 60 TVISKGCSLNC---VDDSDQYV---VGKK-----NITCCDTLCLNKGSAHALQAPAAIIL 109
DB 58 WVFS---NLRCGTPEPCQEAFTNRKGLTYNTTCNKCNCNSAGPRP-TPALGLVFL 113
-----
QY 110 LPAIGLLIL 118
DB 114 TSLAGLGLW 122
-----
RESULT 13
SLUR_MOUSE
ID SLUR_MOUSE STANDARD; PRT; 110 AA.
AC Q920K7;
DT 16-OCT-2001 (Rel. 40, Created)
```

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secreted Ly-6/UPAR related protein 1 precursor (SLURP-1) (ARS
 component B).
 GN SLURP1 OR ARS
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Mastrangelo R., Donini S., Kelton C., Lou S., Serlupi-Crescenzi O.,
 RA Vaccaro R., Renda T., Bressan A., Micangeli E., Milazzo F., Ciolli V.,
 RA Biffoni M., El Tayer N., Lisciani R., Borrelli F., Martelli F.,
 RA Serani S., Papolan R.;
 RT "Cloning of ARS gene, Component B, a new member of Ly-6-related
 family.";
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
 RA Brownstein M. J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamiya M., Lee N. H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
 RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC
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 CC
 CC EMBL; AJ132356; CAA10646.1; -
 CC EMBL; AK003904; BAB23068.1; -
 CC MGP; MGI:1930923; ARS.
 DR InterPro; IPR003632; Ly-6_CD59.
 DR InterPro; IPR001526; Ly6_UPAR.
 DR ProDom; PD003128; Ly-6_CD59; 1.
 DR SMART; SM00134; LU; 1.
 DR PROSITE; PS00983; LY6_UPAR; 1.
 KW Cycokine; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 110 SECRETED LY-6/UPAR RELATED PROTEIN 1.
 FT DOMAIN 24 73 UPAR/LY6.
 FT DISULFID 25 50 POTENTIAL.
 FT DISULFID 28 37 POTENTIAL.
 FT DISULFID 43 73 POTENTIAL.
 FT DISULFID 77 93 POTENTIAL.
 FT DISULFID 94 99 POTENTIAL.
 FT SEQUENCE 110 AA; 12016 MW; AAB69CF6C5F5BFC CRC64;

Query Match 15.4%; Score 99.5; DB 1; Length 110;
 Best Local Similarity 25.8%; Pred. No. 0.0022;
 Matches 25; Conservative 13; Mismatches 42; Indels 17; Gaps 2;
 QY 8 LLMAGIALQPTALLCYSCAKQVSNEDCLOVENCTQLGECQWTARTRAVGLTV----- 61
 DB 10 LLLAAWSMGYGEAPRCYCTQPTAINSKNIAKCKMEDTACKTV-----LETVEAAPPF 63
 QY 62 -----ISKGSLNCVDDSDQYVYVKKNIITCCDDTLN 93
 DB 64 NHSPWTRSCSSCLATDPDGIQVHPVFCFRDLN 100
 RESULT 14
 ID_NKS6_PSETE STANDARD; PRT; 79 AA.
 AC Q9W7J7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin 6 precursor (Alpha neurotoxin 6).
 GN SNTX6
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=9449602; PubMed=10518793;
 RA Gong N. L., Armugam A., Jayaseelan K.;
 RA "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: CDNA
 RT cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 RN [2]
 RP SEQUENCE FROM N.A.; AND IDENTIFICATION OF INTRONS.
 RC TISSUE=Venom gland;
 RX MEDLINE=20279909; PubMed=10818230;
 RA Gong N. L., Armugam A., Jayaseelan K.;
 RA "Molecular cloning, characterization and evolution of the genes
 RT encoding a new group of short-chain alpha-neurotoxins in an Australian
 RL elapid, Pseudonaja textilis.";
 RL FEBS Lett. 473:303-310(2000).
 CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
 CC -1- SIMILARITY: Belongs to the snake toxin family.
 CC
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 CC
 CC EMBL; AF082980; AAD40972.1; -
 CC EMBL; AF204973; AAF75224.1; -
 CC HSSP; P01426; 1NEA.
 DR InterPro; IPR003571; Snake_toxin.
 DR Pfam; PF00087; toxin; 1.
 DR ProDom; PD000206; Snake_toxin; 1.
 DR PROSITE; PS00272; SNAKE_TOXIN; FALSE NEG.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 ACetylcholine receptor inhibitor; Signal; Multigene family.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 79 SHORT NEUROTOXIN 6.
 FT DISULFID 24 41 BY SIMILARITY.
 FT DISULFID 34 51 BY SIMILARITY.
 FT DISULFID 63 71 BY SIMILARITY.

FT DISULFID 72 77 BY SIMILARITY.
SQ SEQUENCE 79 AA; 8570 MW; 73676636A59E947D CRC64;

Query Match 14.9%; Score 96.5; DB 1; Length 79;
Best Local Similarity 31.9%; Pred. No. 0.0032;
Matches 30; Conservative 8; Mismatches 39; Indels 17; Gaps 4;

Qy 1 MKAVLLALLMAG-LALQPGTALLCYSCKAQVSNEDCLQVENCCTQLGECQCTARIRAVGLL 59
Db 1 MKTLLLVMTINCLDGLYLTCT--KSLSGTVVCKPHEFI-----CYRRLIPATHGN 52

Qy 60 TVISKGCSLNCVDSQDYVVGKKNITCCDTDLN 93
Db 53 AIIDRGCSSTC-----PGNRPVCCSTDLN 78

RESULT 15
CD59 PAFSP
ID CD59 PAFSP STANDARD; PRT; 126 AA.
AC Q28785;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN CD59.
OS Papio sp. (Baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=61183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95104908; PubMed=7528724;
RA Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
RA Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
RT "Primate terminal complement inhibitor homologues of human CD59.";
RL Immunogenetics 41:51-51(1995).
CC -!- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
CC COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE CSB-8 STAGE OF MAC
CC ASSEMBLY.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
CC
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CC
CC EMBL; L22862; AAA74127.1; -
CC PIR; I36914; I36914.
CC HSSP; P13987; 1CDS.
DR InterPro; IPR003632; Ly-6 CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_Ly6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; Ly6 UPAR; 1.
KW Antigen; Glycoprotein; GPI-anchor; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 100 CD59 GLYCOPROTEIN.
FT PROPEP 101 126 REMOVED IN MATURE FORM (BY SIMILARITY).
FT DOMAIN 26 106 UPAR/Ly6.
FT DISULFID 28 52 BY SIMILARITY.
FT DISULFID 31 38 BY SIMILARITY.
FT DISULFID 44 64 BY SIMILARITY.
FT DISULFID 70 88 BY SIMILARITY.
FT DISULFID 89 94 BY SIMILARITY.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
* . . . *

FT LIPID 100 100 GPI-ANCHOR (BY SIMILARITY).
SQ SEQUENCE 126 AA; 13716 MW; 7900FF937871EBDC CRC64;

Query Match 14.9%; Score 96.5; DB 1; Length 126;
Best Local Similarity 25.0%; Pred. No. 0.005; Mismatches 42; Indels 41; Gaps 7;
Matches 33; Conservative 16;

Qy 3 AVLLALILMA-GLALQPGTALLCYSCKAQVSNEDCLQVENCCT-----QLGECQ 48
Db 7 SVLFGLLLALAVFCHSGHSLQCYNCNPPTN--CKTAINCSGSGFDTCIARAGLQVYNQC 64

Qy 49 WTARIRAVGLLTVISKCSLNCVD-----DSQDYVVGKKNITCCDTDLN---XSGAHALQ 101
Db 65 WK-----FANCFNFDISTLLKESLQYF-----CCKEDLCNQLENGGTSL 106

Qy 102 PAAAILALLPAL 113
Db 107 EKTVLLLVTPLL 118

Search completed: August 18, 2003, 19:41:56
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:38:29 ; Search time 96 Seconds
(without alignments)
330.630 Million cell updates/sec

Title: US-09-934-586a-2
Perfect score: 646
Sequence: 1 MKAVLLALLMAGLALQPGTA.....AAILLALPALGLLLMGPGQL 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	384	59.4	123	11 Q9D7U0	Q9d7u0 mus musculus
2	144	22.3	136	11 Q99JA5	Q99ja5 mus musculus
3	138.5	21.4	127	11 Q9D2D3	Q9dd23 mus musculus
4	129	20.0	133	11 Q9CXN2	Q9cxn2 mus musculus
5	125	19.3	111	11 Q9CQ11	Q9cq11 mus musculus
6	122	18.9	209	4 Q9IV16	Q9iv16 homo sapien
7	117.5	18.2	141	4 Q96AC2	Q96ac2 homo sapien
8	114.5	17.7	165	4 Q8N2G4	Q8n2g4 homo sapien
9	111.5	17.3	141	11 Q8BLC3	Q8blc3 mus musculus
10	111	17.2	144	5 Q9VIH8	Q9vih8 drosophila
11	111	17.2	160	11 Q8K356	Q8k356 mus musculus
12	110.5	17.1	141	11 Q9J96	Q9jj96 mus musculus
13	106	16.4	189	13 Q9PW14	Q9pw14 cynops pyrr
14	103.5	16.0	185	5 Q9VK99	Q9vk99 drosophila
15	103	15.9	228	11 Q9DIN2	Q9din2 mus musculus
16	101	15.6	135	4 Q8IY94	Q8iy94 homo sapien

17	101	15.6	322	11 Q9R119	Q9r119 cricetus
18	100.5	15.6	135	11 Q63317	Q63317 rattus norv
19	97.5	15.1	425	5 Q9VJ22	Q9vj22 drosophila
20	97	15.0	86	13 Q8AY51	Q8ay51 bungarus ca
21	97	15.0	86	13 Q8AY50	Q8ay50 bungarus ca
22	97	15.0	124	4 Q8TDM5	Q8tdm5 homo sapien
23	96.5	14.9	510	13 Q9FSL9	Q9fsl9 xenopus lae
24	96	14.9	83	13 Q9W716	Q9w716 naja atra (
25	96	14.9	368	5 Q9XVP4	Q9xvp4 caenorhabdi
26	95.5	14.8	504	13 Q13102	Q13102 carassius a
27	95	14.7	222	11 Q91Z14	Q91z14 mus musculu
28	94.5	14.6	128	6 Q8SQ46	Q8sq46 macaca fasc
29	94.5	14.6	128	6 Q8SPI3	Q8spi3 macaca fasc
30	94.5	14.6	493	4 Q8NERS	Q8ners homo sapien
31	94.5	14.6	493	4 Q8TBC2	Q8tbg2 homo sapien
32	93	14.4	86	13 Q8AY49	Q8ay49 bungarus ca
33	93	14.4	154	11 Q9CWP4	Q9cwp4 mus musculu
34	92.5	14.3	140	5 Q9SPN4	Q9spn4 aedes aegyp
35	92.5	14.3	140	5 Q8T4U1	Q8t4u1 aedes aegyp
36	92.5	14.3	159	5 Q8SXW7	Q8sxw7 drosophila
37	92.5	14.3	328	11 Q35771	Q35771 rattus norv
38	92	14.2	134	11 Q63318	Q63318 rattus norv
39	92	14.2	192	13 Q9PW13	Q9pw13 cynops ensi
40	91.5	14.2	365	13 Q91347	Q91347 xenopus lae
41	91.5	14.2	386	13 Q9FSL7	Q9fsl7 xenopus lae
42	91.5	14.2	478	5 Q9W487	Q9w487 drosophila
43	91.5	14.2	493	11 P70539	P70539 rattus norv
44	91.5	14.2	510	13 Q91962	Q91962 xenopus. ac
45	91.5	14.2	510	13 Q9PSL8	Q9psl8 xenopus lae

ALIGNMENTS

RESULT 1

Q9D7U0	ID	Q9D7U0	PRELIMINARY;	PRT;	123 AA.
AC	Q9D7U0;				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
DE	2210408B04R1k	protein (Prostate stem cell antigen).			
GN	PCSA OR 2210408B04R1K.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Stomach;				
RC	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,				
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,				
RA	Sadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaio M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaets P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,				
RT	Hayashizaki Y.;				
RL	"Functional annotation of a full-length mouse cDNA collection.;"				
RL	Nature 409:685-690(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				

```
RC STRAIN=C57BL/6;
RX MEDLINE=21371909; PubMed=11479226;
RA Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
RT "Murine six-transmembrane epithelial antigen of the prostate, prostate
RT stem cell antigen, and prostate-specific membrane antigen: prostate-
RT specific cell-surface antigens highly expressed in prostate cancer of
RT transgenic adenocarcinoma mouse prostate mice.";
RL Cancer Res. 61:5857-5860(2001).
DR EMBL; AK008851; BAB25929.1; -
DR EMBL; AF319173; AAK84073.1; -
DR HSSP; P13987; IERG.
DR MGD; MGI:1919623; Peca.
DR InterPro; IPR003632; Lv-6_CD59.
DR InterPro; IPR001526; LY6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
DR PROSITE; PS00983; LY6_UPAR; 1.
SQ SEQUENCE 123 AA; 13477 MW; 67A8566F3D30797A CRC64;

Query Match 59.4%; Score 384; DB 11; Length 123;
Best Local Similarity 57.7%; Pred. No. 2.6e-37;
Matches 71; Conservative 16; Mismatches 36; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQLGEOCWTARIRAVGLLT 60
Db 1 MKTVFFLLATYLLAHFGAALQCYSCTAQMNRRDCLNVONCSLDQHSCTFSRIRAGLVT 60

Qy 61 VISKGSCLNCVDDSDQDYVYVGGKKNITCCDPTDLCNKGSAHALQPAALALLPALGLLLWGP 120
Db 61 VISKGSQCCEDDSENYVYVGGKKNITCCVSDLCNVNGAHTLPPPTTGLTLLVCSLLWGS 120

Qy 121 GQL 123
Db 121 SRL 123

RESULT 2
Q99JA5 PRELIMINARY; PRT; 136 AA.
AC Q99JA5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lymphocyte antigen 6 complex, locus E.
GN LY65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005684; AAH05684.1; -
DR EMBL; BC002116; AAH02116.1; -
DR EMBL; BC003926; AAH03926.1; -
DR EMBL; BC019113; AAH19113.1; -
DR MGD; MGI:106651; Lyce.
DR InterPro; IPR003632; LY-6_CD59.
DR InterPro; IPR001526; LY6_UPAR.
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DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 136 AA; 14392 MW; 5A1CBBE1464DC029 CRC64;

Query Match 22.3%; Score 144; DB 11; Length 136;
Best Local Similarity 30.8%; Pred. No. 5.1e-09;
Matches 40; Conservative 20; Mismatches 60; Indels 10; Gaps 3;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQLGEOCWTARIRAVGLLT 110
Db 7 MRVFLPVLLAALLGMEQVHSLCMFCSDTDQKNINCLNLPVSCQEKDHYCITLSAAGFGNV 66

Qy 57 GLLTVISKGSCLNCVDDSDQDYVYVGGKKNITCCDPTDLCNKGSAHALQPAALALLPALGL 110
Db 67 NLGYTLNKGSPICPSNVNVLNLGVSNSVCCQSSFCNFSAGLGLURASIPLLGLGLLL 126

Qy 111 PALGLLLWGP 120
Db 127 SLLALLQLSP 136

RESULT 3
Q9DD23 PRELIMINARY; PRT; 127 AA.
AC Q9DD23;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 0610005K03RIK protein.
GN 0610005K03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002226; BAB21948.1; -
DR HSSP; P13987; IERG.
DR MGD; MGI:1915561; 0610005K03RIK.
DR InterPro; IPR003632; LY-6_CD59.
DR InterPro; IPR001526; LY6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; LY-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 127 AA; 13279 MW; 9CCE20688671882C CRC64;

Query Match 21.4%; Score 138.5; DB 11; Length 127;
Best Local Similarity 31.4%; Pred. No. 2.1e-08;
Matches 38; Conservative 24; Mismatches 48; Indels 11; Gaps 5;
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Qy 4 VLLALLMAGLALQPGTALLCYSCQAQVSNEDCLOVENCTOLGEOCWTARAVGLL---- 59
Db 7 VLLALIL-GTRELAMALQYVCANPVSASCTVTHC-HINETMCKTTLTSLVPPFL 64

Qy 60 --TVISKGSLSNVDDSDQYVVGKNITCCDIDLNCXSGAHL-OPAAAILALLPALGLL 116
Db 65 GDSIVTKSKASCPSDVGIGQTRPVSNCNSDLNVDGAPSLGPGLLALL--ALFLL 122

Qy 117 L 117
Db 123 L 123

RESULT 4
Q9CXN2 PRELIMINARY; PRT; 133 AA.
AC Q9CXN2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Lymphocyte antigen 6 complex, locus E.
GN Ly6E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirln L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018552; BAB32171.1; -.
DR EMBL; AK008365; BAB25630.1; -.
DR MGD; MGI:1914288; 2010109103Rik.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 133 AA; 14441 MW; 8FCF9D4EDA457255 CRC64;

Query Match 20.0%; Score 129; DB 11; Length 133;
Best Local Similarity 30.7%; Pred. No. 2.9e-07;
Matches 31; Conservative 19; Mismatches 45; Indels 6; Gaps 2;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCQAQVSNEDCLOVENCTOLGEOCWTARIRA---V 56
Db 7 MRVFLVLLALLMAGLALQPGTALLCYSCQAQVSNEDCLOVENCTOLGEOCWTARIRA---V 66

Qy 57 GLLTVISKGSLSNVDDSDQYVVGKNIT--CCDIDLNCXNS 95
Db 67 NLGYTLNKGCSPICPSENVLNLGWSVNSYCCQSSFCNFS 107

RESULT 5

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Q9CQ11 PRELIMINARY; PRT; 111 AA.
AC Q9CQ11;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 2010109103Rik protein.
GN 2010109103RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Colon, and Small intestine;
MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirln L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK018552; BAB32171.1; -.
DR EMBL; AK008365; BAB25630.1; -.
DR MGD; MGI:1914288; 2010109103Rik.
DR InterPro; IPR003632; Ly-6_CD59.
DR InterPro; IPR001526; Ly6_UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR ProDom; PD003128; Ly-6_CD59; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 111 AA; 12280 MW; DB0138AE7094D321 CRC64;

Query Match 19.3%; Score 125; DB 11; Length 111;
Best Local Similarity 31.4%; Pred. No. 7e-07;
Matches 33; Conservative 16; Mismatches 46; Indels 10; Gaps 4;

Qy 5 LLALLMAGLALQPGTALLCYSCQAQVSNEDCLOVENCTOLGEOCWTARIRAVGLLTWISK 64
Db 8 LLPILLGSSAQ---ALKCHECS---GIEDCYKPKTCTSSQSLYCLTNWYPPGQTTVK 61

Qy 65 GCSLNCVDDSDQYVVGKNITCCDIDLNCXSGAHLQPAAILAL 109
Db 62 TCAYTCPD--INHVTANSKSSCCNTDLN--SARNLHVSGLLAL 102

RESULT 6
Q8IV16 PRELIMINARY; PRT; 209 AA.
AC Q8IV16;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.

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RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035810; AAH35810.1; -.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 209 AA; 23320 MW; 1F3A2B890CEA6724 CRC64;

Query Match 18.9%; Score 122; DB 4; Length 209;
Best Local Similarity 24.2%; Pred. No. 3.1e-06;
Matches 43; Conservative 18; Mismatches 49; Indels 68; Gaps 5;

Qy 3 AVLLALLMAGLALQPG-----TA 20
Db 31 AVLLALLCG---RPRGQTQEEEDHDPDDYDEEDEVETNRLPGRSRVL 87

Qy 21 LLCYSCKAQVSNEDCLQVNTQGEQCWTARIRA---VGLLTVISKCSLNCVDDSDQY 77
Db 88 LRCYTCKSLPRDRCNLITQNGSH-GQTCTTLIAHGNTESGLLTHSTWCTDSCQPIKTV 146

Qy 78 YVGKKNITCCDIDLCKN-----SGAHALQPAALALLPALGLL 116
Db 147 EGTQVTTCOSSLNCNPPWQSSRVQDPTGKGAGGRGSSSETVGAALLNLLAGLGAM 204

RESULT 7
Q96AC2 PRELIMINARY; PRT; 141 AA.
AC Q96AC2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Hypothetical protein FLJ37182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017318; AAH17318.1; -.
KW Hypothetical protein.
SQ SEQUENCE 141 AA; 15240 MW; CFA6D98BA90792E3 CRC64;

Query Match 18.2%; Score 117.5; DB 4; Length 141;
Best Local Similarity 32.8%; Pred. No. 6.9e-06;
Matches 43; Conservative 13; Mismatches 54; Indels 21; Gaps 7;

Qy 6 LALLMAGLALQPGTAL--LCYSCKAQVSNEDCLQVE---NCT-OLGECQWTARI-RAVGL 58
Db 6 IAATFCGLFWLPGALQIQCYQCEEFQLNNDCCSPFIVNCTVNVQDMCQKEVMEQSAGI 65

Qy 59 LTVISKGCSLNCVDDSDQY----VGKKN---ITCCDTDLN-----XSGAHALQPA 104
Db 66 MYRKSASSAACLIATASAGYQSCFPGKLSVCISCCNTPLCNGPRPKRGSSASALRPL 125

Qy 105 AILALLPALGL 115
Db 126 RTTILFLKIAL 136

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RESULT 8
Q8N2G4 PRELIMINARY; PRT; 165 AA.
AC Q8N2G4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein OVARC1001499.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075487; BAC11647.1; -.
KW Hypothetical protein.
SQ SEQUENCE 165 AA; 17900 MW; 2B0B8D68044C8999 CRC64;

Query Match 17.7%; Score 114.5; DB 4; Length 165;
Best Local Similarity 33.9%; Pred. No. 1.9e-05;
Matches 40; Conservative 13; Mismatches 44; Indels 21; Gaps 7;

Qy 6 LALLMAGLALQPGTAL--LCYSCKAQVSNEDCLQVE---NCT-OLGECQWTARI-RAVGL 58
Db 6 IAATFCGLFWLPGALQIQCYQCEEFQLNNDCCSPFIVNCTVNVQDMCQKEVMEQSAGI 65

Qy 59 LTVISKGCSLNCVDDSDQY----VGKKN---ITCCDTDLN-----XSGAHALQ 102
Db 66 MYRKSASSAACLIATASAGYQSCFPGKLSVCISCCNTPLCNGPRPKRGSSASALRPL 123

RESULT 9
Q8BLC3 PRELIMINARY; PRT; 141 AA.
AC Q8BLC3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical snake toxin-like structure containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK045592; BAC32428.1; -.
KW Hypothetical protein.
SQ SEQUENCE 141 AA; 15261 MW; 51717F7922C02DAA CRC64;

Query Match 17.3%; Score 111.5; DB 11; Length 141;
Best Local Similarity 31.6%; Pred. No. 3.5e-05;
Matches 42; Conservative 14; Mismatches 56; Indels 21; Gaps 7;

Qy 6 LALLMAGLALQPGTAL--LCYSCKAQVSNEDCLQVE---NCT-OLGECQWTARI-RAVGL 58
Db 6 IAATFCGLFWLPGALQIQCYQCEEFQLNNDCCSPFIVNCTVNVQDMCQKEVMEQSAGI 65

Qy 59 LTVISKGCSLNCVDDSDQY----VGKKN---ITCCDTDLN-----XSGAHALQPA 104

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Db 66 MYRSCASSAALIASAGYQSCFGKLNVCISCCNTPLCNGPRPKRGSSAIRPGL 125
QY 105 AIALALLPALGLLL 117
Db 126 LTTLLFHLALCL 138

RESULT 10
Q9VIH8
ID Q9VIH8 PRELIMINARY; PRT; 144 AA.
AC Q9VIH8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE CG14401 protein.
GN CG14401
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbini K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foeller C., Gabrielian A.A., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiambs I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AB003668; AAF53941.1; -.
DR FlyBase; FBgn032900; CG14401.
SQ SEQUENCE 144 AA; 15055 MW; A32C221F07E0860F CRC64;

Query Match 17.2%; Score 111; DB 5; Length 144;
Best Local Similarity 27.3%; Pred. No. 4.1e-05;
Matches 39; Conservative 15; Mismatches 61; Indels 28; Gaps 6;

QY 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCNTQLGECQWTRIRAVGLLT 47

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Db 1 MMAALASLFLVLTVLASSARAITCECDVSNVPGCFVGGDDISTTDCDVANNRSLGAE 60
QY 48 --CWTARIRAV-GLLTVISKGC-----SLNCVDDSDQDYVYKKNI---TCDDTDLGN 93
Db 61 ATCLTKYHEGMPGDTFRVRSYFGDASPIGVSC-DDGPDVFPVFMFLGCTLCDTDLGN 119
QY 94 XSGAHLQPAALALPALGLL 116
Db 120 AAAGLSTPLVIALSLGLLVLL 142

RESULT 11
Q8K356
ID Q8K356 PRELIMINARY; PRT; 160 AA.
AC Q8K356;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to lymphocyte antigen 6 complex, locus H.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028758; AAH28758.1; -.
DR InterPro; IPR001526; LY6 UPAR.
DR Pfam; PF00021; UPAR_LY6; 1.
DR SMART; SM00134; LU; 1.
SQ SEQUENCE 160 AA; 17028 MW; 01536076672DCD75 CRC64;

Query Match 17.2%; Score 111; DB 11; Length 160;
Best Local Similarity 29.7%; Pred. No. 4.6e-05;
Matches 41; Conservative 16; Mismatches 59; Indels 22; Gaps 7;

QY 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCNTQLGECQWTRIRAVGLLT 60
Db 27 MKSLGLALLALLCPSPAHGLWCQDC--TLNASHHCAKQCQPTDTVCASVRITDSSSR 84
QY 61 ---VISKGCSLNCVDD-----SQDYVVG-----KKNITCCDDTDLNCSGAHALQPA 104
Db 85 KDSVNVKVCASSC--DEVKHFSTDYLMGINSILKVDVDCCKDLNCSVAGRSFWA 142
QY 105 AIALALPALG-LLLM-GP 120
Db 143 LAGLLLSLGLPALIWAGP 160

RESULT 12
Q9JJ96
ID Q9JJ96 PRELIMINARY; PRT; 141 AA.
AC Q9JJ96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Brain cDNA, clone MNCB-0671.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library
made by oligo-capping method."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041649; BAA95101.1; -.

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RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003635; AAF53179.2; -

DR FlyBase; FBgn0032422; CG6579.

SQ SEQUENCE 185 AA; 20370 MW; 8BECDA1A55414BE2 CRC64;

Query Match

Best Local Similarity 16.0%; Score 103.5; DB 5; Length 185;

Matches 35; Conservative 26; Mismatches 47; Indels 43; Gaps 6;

QY 1 MKAVLLALLMAGLALQPGTALLCYSCKA-----QVSNEDCLQVENCITQLGEQCWTA 51

Db 44 LKQVIFVLLIAVCTMHSASAIKCYQCKSLTDPNCAKDIDSASINRAVDCDSVPEKPTME 103

QY 52 RIRAVGLL-----TWISKGCSLNCVDDSDQDYVVGKKNITC-----CD 88

Db 104 QLQPVTRCNKVTSDRAGTIVSRDCHPES-----IGQKNECTVTHSRQVESCCTCK 155

QY 89 TDLGNXSGA--HALQPAALALPALGLLL 117

Db 156 GDLGNASGAGRFVAVSATALAIL-ALNLSL 185

RESULT 15

Q9DIN2

ID Q9DIN2 PRELIMINARY; PRT; 228 AA.

AC Q9DIN2;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE 1110002J19RIK protein (High density lipoprotein binding protein

DE 1).

GN 1110002J19RIK OR HBPI.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.;"

RL Nature 409:685-690(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Ioka R.X., Kang M., Kim D., Fujino T., Yamamoto T.T.;

RT "High Density Lipoprotein Binding Protein 1.;"

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK003305; BAB22704.1; -

DR EMBL; AB095543; BAC23061.1; -

DR MGD; MGI:1915703; 1110002J19RIK.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR001526; LY6_UPAR.

DR Pfam; PF00021; UPAR_LY6; 1.

DR SMART; SM00134; LU; 1.

DR PROSITE; PS00290; IG_MHC; 1.

DR PROSITE; PS00983; LY6_UPAR; 1.

KW Lipoprotein.

SQ SEQUENCE 228 AA; 24566 MW; B2FB456A10865EB1 CRC64;

Query Match

Best Local Similarity 15.9%; Score 103; DB 11; Length 228;

Matches 33; Conservative 14; Mismatches 43; Indels 46; Gaps 3;

QY 1 MKAVLLALLMAGLALQPGTA----- 20

Db 4 LRAVLLILLLSG---QPGSGWAQEDGDADPEPENYNVDDDDDEEBEETNIPGSRDRAP 60

QY 21 LLCYSCKAQVSNEDCLQVENCITQLGEQCWTARIRA---VGLLTIVISKGCSLNCVDDSDQDY 77

Db 61 LCYFCQVLSHSGSCNQTSQSSSKPFCITLVSHSGTDKGYLTYSNMWCTDTTCQPIIKTV 120

QY 78 YVGKKNITCCDTLGN 93

Db 121 GGTQMTQTCCQSTLGN 136

Search completed: August 18, 2003, 19:43:39

Job time : 97 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:38:54 ; Search time 39 Seconds
(without alignments)
303.301 Million cell updates/sec

Title: US-09-934-586A-2

Perfect score: 646

Sequence: 1 MKAVLLALLMAGLALQPGTA.....AAILALLPALGLLWPGQL 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144	22.3	136	2 I49013	thymic shared anti
2	126	19.5	127	1 A46528	phosphatidylinositol
3	126	19.5	130	2 I54553	gene ThB protein -
4	121.5	18.8	103	2 A59031	AKS component B 81
5	100.5	15.6	135	2 A45835	Ly6 homolog RK10 p
6	96.5	14.9	126	2 I36914	CD59 protein - bab
7	96.5	14.9	510	1 A42635	activin receptor S
8	96	14.9	368	2 T21748	hypothetical prote
9	95	14.7	128	1 A57321	E48 antigen precu
10	95	14.7	222	2 B41643	urokinase-type pla
11	95	14.7	222	2 B55356	urokinase-type pla
12	95	14.7	327	2 A55356	urokinase-type pla
13	94.5	14.6	126	2 S53340	CD59 protein - rat
14	94	14.6	504	2 B40829	activin receptor i
15	94	14.6	528	2 C40829	activin receptor i
16	93	14.4	83	2 S70374	cardiotoxin V prec
17	92.5	14.3	128	1 RWHU59	surface glycoprote
18	92.5	14.3	328	2 S42152	urinary plasminoge
19	92	14.2	134	2 D45835	Ly6 homolog RK3 pr
20	91.5	14.2	365	2 S27268	activin receptor S
21	91.5	14.2	510	1 A56926	activin receptor i
22	91	14.1	512	2 I37134	activin type II re
23	90	13.9	246	2 B37225	acrosomal protein
24	90	13.9	512	2 D40829	activin receptor i
25	90	13.9	513	2 J01484	activin receptor p
26	90	13.9	536	2 A40829	activin receptor i
27	89.5	13.9	285	2 I77964	SP-10 - western ba
28	89	13.8	251	2 I57999	SP-10 - western ba
29	88.5	13.7	265	2 A37225	acrosomal protein

30 86 13.3 527 2 A54985
31 85 13.2 86 1 V6EP9A
32 85 13.2 86 2 A37910
33 85 13.2 570 2 I45712
34 84 13.0 128 2 I36894
35 82 12.7 131 2 I56894
36 81 12.5 82 2 JC5892
37 81 12.5 1291 2 T13389
38 80.5 12.5 82 2 S70375
39 80.5 12.5 261 2 I52518
40 79.5 12.3 65 2 S67985
41 79.5 12.3 83 2 SI9951
42 77 11.9 73 1 N2NJ1R
43 76.5 11.8 342 2 T22167
44 76.5 11.8 2823 2 T23064
45 76.5 11.8 2823 2 F87908

ALIGNMENTS

RESULT 1

I49013

thymic shared antigen-1 - mouse

N;Alternate names: Sca-2 precursor; TSA-1

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I49013; I48910

R;MacNeil, I.; Kennedy, J.; Godfrey, D.I.; Jenkins, N.A.; Masciantonio, M.; Mineo, C.;

J. Immunol. 151, 6913-6923, 1993

A;Title: Isolation of a cDNA Encoding Thymic Shared Antigen-1: A New Member of the Ly6 F

A;Reference number: I49013; MUID:94081342; PMID:8258699

A;Accession: I49013

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-136 <RES>

A;Cross-references: EMBL:U09192; NID:G487390; PIDN:AAB03366.1; PID:G487391

R;Classon, B.J.; Coverdale, L.

Proc. Natl. Acad. Sci. U.S.A. 91, 5296-5300, 1994

A;Title: Mouse stem cell antigen Sca-2 is a member of the Ly-6 family of cell surface pr

A;Reference number: I48910; MUID:94261572; PMID:8202484

A;Accession: I48910

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-136 <RE2>

A;Cross-references: EMBL:U04268; NID:G434659; PIDN:AAA19121.1; PID:G434660

C;Comment: This belongs to the Ly-6 family, a group of small cysteine-rich cell surface

C;Superfamily: Ly-6 antigen; Ly-6 homology

Query Match 22.3%; Score 144; DB 2; Length 136;

Best Local Similarity 30.8%; Pred. No. 8.7e-07;

Matches 40; Conservative 20; Mismatches 60; Indels 10; Gaps 3;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLOVENCQTOLGEOCWTAIRIA----V 56

Db 7 MRVFLPVLLAALLGMEQVHSLMFCSTCDQNNINCLMPVSCQEKDHYVCITLSAAAGFGNV 66

Qy 57 GLLTVISKGSCLNCVDSDQYVYVKKNIT--CCDTDLCKXS---GAHALQPAAILALL 110

Db 67 NLGYTLNKGCSPTCPSENVLNLGVASVNSYCCQSFNFSAGLGLURASIPILGLGLLL 126

Qy 111 PALGLLLWGP 120

Db 127 SLALLQLSP 136

RESULT 2

A46528

phosphatidylinositol-anchored B-cell antigen ThB precursor - mouse

N;Alternate names: thymocyte B-cell antigen ThB

C;Species: Mus musculus (house mouse)

C;Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 28-Jan-2000

C;Accession: A46528

R;Gumley, T.P.; McKenzie, I.F.; Kozak, C.A.; Sandrin, M.S.
J. Immunol. 149, 2615-2618, 1992
A:Title: Isolation and characterization of cDNA clones for the mouse thymocyte B cell antigen 127
A:Reference number: A46528; MUID:93017863; PMID:1401899
A:Accession: A46528
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127 <GUM>
A:Cross-references: GB:X63782; GB:S46666; NID:G288264; PIDN:CAA45317.1; PID:G288265
A:Experimental source: C57BL/6, spleen cells, thymocytes
A:Note: sequence extracted from NCBI backbone (NCBI:P:116104)
C:Comment: This 15K GPI-anchored surface antigen is found on B thymocytes and B cells.
C:Genetics:
A:Gene: Thb
A:Map position: 15
C:Superfamily: Ly-6 antigen; Ly-6 homology
F:1-20/Domain: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F:21-100/Domain: signal sequence #status predicted <SIG>
F:21-93/Product: phosphatidylinositol-anchored B-cell antigen Thb #status predicted <MAT>
F:94-127/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
Query Match 19.5%; Score 126; DB 1; Length 127;
Best Local Similarity 31.8%; Pred. No. 4.3e-05;
Matches 42; Conservative 19; Mismatches 51; Indels 20; Gaps 7;
Qy 1 MKAVLLALLMAGLALQPTALLCYSCKAQVSNEDCLQVENCQTQGEQCWTARIRAVGLL- 59
Db 1 MKTALLVLLVAVATSPAWLRCHVC---TNSANKNPQVCPSNFYFCKT--VTSVEPLN 55
Qy 60 -TVISKGSLNCVDD-SQDYV--GKKNIITCCDIDLNCN-----XSGAHALOPA-----AA 105
Db 56 GNLVRKCANCTSDYSQQGVSSGSEVTQCCQTDLCNRLVSAAPGHALLSSVTGLAT 115
Qy 106 ILALLPALGLLL 117
Db 116 SLSLLTVMALCL 127
RESULT 3
154553
gene Thb protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I54553
R;Gumley, T.P.; McKenzie, I.F.; Sandrin, M.S.
Immunogenetics 42, 221-224, 1995
A:Title: Sequence and structure of the mouse Thb gene.
A:Reference number: I54553; MUID:95369850; PMID:7642235
A:Accession: I54553
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-130 <RES>
A:Cross-references: GB:L40419; NID:G1019624; PIDN:AAA79249.1; PID:G1019625
C:Genetics:
A:Gene: Thb
A:Introns: 21/1; 54/1
C:Superfamily: Ly-6 antigen; Ly-6 homology
F:24-103/Domain: Ly-6 homology <LY6>
Query Match 19.5%; Score 126; DB 2; Length 130;
Best Local Similarity 31.8%; Pred. No. 4.4e-05;
Matches 42; Conservative 19; Mismatches 51; Indels 20; Gaps 7;
Qy 1 MKAVLLALLMAGLALQPTALLCYSCKAQVSNEDCLQVENCQTQGEQCWTARIRAVGLL- 59
Db 4 MKTALLVLLVAVATSPAWLRCHVC---TNSANKNPQVCPSNFYFCKT--VTSVEPLN 58
Qy 60 -TVISKGSLNCVDD-SQDYV--GKKNIITCCDIDLNCN-----XSGAHALOPA-----AA 105
Db 59 GNLVRKCANCTSDYSQQGVSSGSEVTQCCQTDLCNRLVSAAPGHALLSSVTGLAT 118

Qy 106 ILALLPALGLLL 117
Db 119 SLSLLTVMALCL 130
RESULT 4
A59031
ARS component B 81/S protein precursor - human
N:Alternate names: secreted Ly-6/uPAR related protein 1; SLURP-1
C:Species: Homo sapiens (man)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 29-Oct-1999
C:Accession: A59031; A58842
R;Mastrangeli, R.
submitted to the EMBL Data Library, August 1996
A:Description: ARS gene, component B.
A:Reference number: A59031
A:Accession: A59031
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-103 <MAS>
A:Cross-references: GB:X99977; NID:G1536901; PIDN:CAA68237.1; PID:e265523; PID:G1536902
A:Experimental source: placenta
R;Adermann, K.; Wattler, F.; Wattler, S.; Heine, G.; Meyer, M.; Forstmann, W.G.; Nehls, submitted to the Protein Sequence Database, July 1998
A:Description: Secreted protein, related to Ly-6, uPAR, soluble CD59, and snake and frog
A:Reference number: A58842
A:Accession: A58842
A:Molecule type: protein
A:Residues: 23-103 <ADE>
C:Genetics:
A:Gene: ARS
A:Introns: 20/1; 60/1
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-22/Domain: propeptide #status predicted <PRO>
F:23-103/Product: ARS component B 81/S protein #status experimental <MAT>
F:25-50,28-37,94-99/Disulfide bonds: #status experimental
F:43-77,73-93/Disulfide bonds: (or 43-73, 77-93) #status experimental
F:64/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 18.8%; Score 121.5; DB 2; Length 103;
Best Local Similarity 29.7%; Pred. No. 9.8e-05;
Matches 27; Conservative 13; Mismatches 46; Indels 5; Gaps 1;
Qy 8 LLWAGLALQPTALLCYSCKAQVSNEDCLQVENCQTQGEQCWTARIRA-----VGLLTVI 62
Db 10 LLVAWSMGCEALCKYTCRTPMTSASCRITTRCKPBDTACMTTLVTVEAEYFPNQSPV 69
Qy 63 SKGSLNCVDDSQDYVVGKKNITCCDIDLNCN 93
Db 70 TRCSSCVATDPDSIGAHLIFCCFIDLNCN 100
RESULT 5
A45835
Ly6 homolog RK10 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 31-Jan-2000
C:Accession: A45835; B45835
R;Friedman, S.; Pallfree, R.G.E.; Sirlin, S.; Haemmerling, U.
Immunogenetics 31, 104-111, 1990
A:Title: Analysis of three distinct Ly6-A-related cDNA sequences isolated from rat kidney
A:Reference number: A45835; MUID:90152758; PMID:2154400
A:Accession: A45835
A:Molecule type: mRNA
A:Residues: 1-135 <PRI>
A:Cross-references: GB:M30689; NID:G205247; PIDN:AAA41546.1; PID:G205248
A:Experimental source: clone RK10
A:Accession: B45835
A:Molecule type: mRNA
A:Residues: 25-54, 'A', 56-62, 'M', 64-67, 'Q', 69-71, 'DHI', 75-77, 'V', 79-80, 'T', 82-85, 'T', 87, 'A';
A:Cross-references: GB:M30692; NID:G205245; PIDN:AAA41545.1; PID:G205246
A:Experimental source: clone RK6

C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F;1-26/Domain: signal sequence #status predicted <SIG>
F;106/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match 15.6%; Score 100.5; DB 2; Length 135;
Best Local Similarity 30.8%; Pred. No. 0.013;
Matches 32; Conservative 10; Mismatches 53; Indels 9; Gaps 3;

Qy 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCQTQGEQWTRARAVGL-- 58
Db 7 MKSCVLLALLCAERAQGLNLCYNCIMPGNTCSSTATCPYPDGVCTQVAEYVSS 65
Qy 59 --LTVISKGSLNCDVDSQD----YYVGKKNITCCDIDLGNXSG 96
Db 66 VRLVKVSNLCLPGCKPQPEVLGTGVHVNTDCCNTDLCLNAG 109

RESULT 6

I36914
C;Species: Papio sp. (baboon)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: I36914
R;Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, E.R.; Rother, R.
Immunogenetics 41, 51, 1995
A;Title: Primate terminal complement inhibitor homologues of human CD59.
A;Reference number: I36894; MUID:95104908; PMID:7528724
A;Accession: I36914
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-126 <RES>
A;Cross-references: GB:I22862; NID:G514327; PIDN:AAA74127.1; PID:G514328
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-100/Domain: Ly-6 homology <Ly6>

Query Match 14.9%; Score 96.5; DB 2; Length 126;
Best Local Similarity 25.0%; Pred. No. 0.029;
Matches 33; Conservative 16; Mismatches 42; Indels 41; Gaps 7;

Qy 3 AVLLALLMA-GLALQPGTALLCYSCKAQVSNEDCLQVENC-----QLGEQC 48
Db 7 SVLFGLLLALAVFCHGSLQCYNCPTTN--CKTAINCSSGPDTCILIRAGLQVYNQC 64
Qy 49 WTARIRAVGLLTVISKGSLNCDVDSQDYYVGKKNITCCDIDLGN--XSGHAHQ 101
Db 65 WK-----FANCFNDISTLLKESLQYF-----CKKEDLCNEQLNGGTSL 106

Qy 102 PAAAILALLPAL 113

Db 107 EKTVLLLVTPLL 118

RESULT 7

A42635
activin receptor STK8 precursor - African clawed frog
N;Alternate names: ActRIIB
N;Contains: protein kinase STK8 (EC 2.7.1.-)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 04-Mar-1993 #sequence_revision 19-Oct-1995 #text_change 13-Jun-1997
C;Accession: A42635; S21233
R;Mathews, L.S.; Vale, W.W.; Kintner, C.R.
Science 255, 1702-1705, 1992
A;Title: Cloning of a second type of activin receptor and functional characterization in
A;Reference number: A42635; MUID:92205349; PMID:1313188
A;Accession: A42635
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-510 <MATH>
A;Cross-references: GB:M88594
A;Experimental source: embryo
A;Note: sequence extracted from NCBI backbone (NCBIP:93126)
R;Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.

FEBS Lett. 303, 81-84, 1992
A;Title: Multiple genes for Xenopus activin receptor expressed during early embryogenesis
A;Reference number: S21171; MUID:92275088; PMID:1317302
A;Accession: S21233

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-510 <NIS>

C;Superfamily: activin receptor II; protein kinase homology

C;Keywords: ATP; glycoprotein; phosphotransferase; receptor; serine/threonine-specific p

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-510/Product: activin receptor II #status predicted <MAT>

F;136-157/Domain: extracellular #status predicted <EXT>

F;158-510/Domain: transmembrane #status predicted <TMI>

F;186-483/Domain: intracellular #status predicted <INT>

F;195-202/Region: protein kinase homology <KIN>

F;43,66/Binding site: protein kinase ATP-binding motif

F;215/Active site: Lys #status predicted

F;43,66/Binding site: carboxylate (Asn) (covalent) #status predicted

F;215/Active site: Lys #status predicted

Query Match 14.9%; Score 96.5; DB 1; Length 510;

Best Local Similarity 26.4%; Pred. No. 0.099;

Matches 37; Conservative 22; Mismatches 50; Indels 31; Gaps 8;

Qy 4 VLIALMAGLALPGTALLC--YSCKAQVSNEDCLQVENCQTQGEQ-----CWTARAV 56

Db 11 LLLATFRAGSGHDEVETRECIYYNANWELEKTNQSGVSECE--GEKDKRLHCVASWRNNS 68

Qy 57 GLLTIVISKGSL--NCVDSQDYYVGKKN-----ITCCDIDLGNXSGAH-----AL 100

Db 69 GFIELVKKGCWLDNFNCY-DRQCIKAENPQVFFCCGECGNYCNKKFTHLPEVETFPDKP 127

Qy 101 QPAAAIL-----ALLPALGL 115

Db 128 QPSASVNLILYSLPIVGL 147

RESULT 8

T21748

hypothetical protein F35C12.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T21748

R;Baynes, C.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19468

A;Accession: T21748

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-368 <WIL>

A;Cross-references: EMBL:Z81075; PIDN:CAR03048.1; GSPDB:GN00019; CESP:F35C12.3

A;Experimental source: clone F35C12

C;Genetics:

A;Gene: CESP:F35C12.3

A;Map position: 1

A;Introns: 53/3; 83/3; 151/3; 167/2; 198/3; 246/3; 281/2

Query Match

14.9%; Score 96; DB 2; Length 368;

Best Local Similarity 30.9%; Pred. No. 0.083;

Matches 21; Conservative 10; Mismatches 31; Indels 6; Gaps 1;

Qy 40 NCTQLGQCQWTRARAVGLLTVISKGSLNCDVDSQDYYVGK-----NITCCDIDLGN 93

Db 214 NCENSGAYCYNMTASASLIEVTKAGCSMRCPAQNKICIGTTTQNPISLCCCTPLCN 273

Qy 94 XSGHAHQ 101

Db 274 AGGEGAIQ 281

RESULT 9

A57321

E48 antigen precursor - human

N;Alternate names: desmoglein III

QY 2 KAVILLAILMAGIALQPGTALLCYSCKAQSVEDNCLOVENTQJGEOCWTAIRA---VGL 58

DB 5 RRLILLILLATTCVPASOGLOCMOE---SNOSCL-VEECALQODLCRTTVLREWQDRE 60

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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:41:59 ; Search time 23 Seconds
(without alignments)
139.807 Million cell updates/sec

Title: US-09-934-586A-2

Perfect score: 646

Sequence: 1 MKAVLLALLMAGLALQPETA.....AAILALLPALGLLLWSPGSQL 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 123791 seqs, 26142687 residues

Total number of hits satisfying chosen parameters: 123791

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	441	68.3	88	6	US-10-631-402-2576
2	441	68.3	88	6	US-10-631-441-2576
3	158.5	24.5	131	1	PCT-US02-29560A-346
4	158.5	24.5	131	7	US-60-485-450-1070
5	158.5	24.5	131	7	US-60-490-890-1489
6	128.5	19.9	116	6	US-10-286-897-2973
7	128.5	19.9	116	6	US-10-258-898A-2973
8	128.5	19.9	128	6	US-10-286-897-6545
9	128.5	19.9	128	6	US-10-258-898A-6545
10	117.5	18.2	141	1	PCT-US03-18400-14
11	117.5	18.2	141	1	PCT-US02-29560A-322
12	117.5	18.2	141	7	US-60-490-890-1833
13	104.5	16.2	162	1	PCT-US03-21703-97
14	102.5	15.9	227	1	PCT-US03-18400-17
15	101	15.6	125	6	US-10-621-401-169
16	97.5	15.1	146	1	PCT-US03-21703-100
17	96.5	14.9	86	7	US-60-485-450-1071
18	95.5	14.8	94	6	US-10-273-573-7711
19	92.5	14.3	128	6	US-10-408-765A-1118
20	91.5	14.2	191	6	US-10-273-573-7712
21	90	13.9	155	1	PCT-US03-21703-86
22	90	13.9	176	1	PCT-US03-21703-83
23	90	13.9	248	6	US-10-273-573-7513
24	88.5	13.7	174	1	PCT-US03-21703-93
25	88.5	13.7	195	1	PCT-US03-21703-90
26	88.5	13.7	195	1	PCT-US03-21703-104

27 84 13.0 123 6 US-10-286-897-3096 Sequence 3096, Ap
28 84 13.0 123 6 US-10-258-898A-3096 Sequence 3096, Ap
29 80 12.4 119 6 US-10-286-897-6668 Sequence 6668, Ap
30 80 12.4 119 6 US-10-258-898A-6668 Sequence 6668, Ap
31 78.5 12.2 78 1 PCT-US03-21703-87 Sequence 87, Appl
32 78.5 12.2 78 1 PCT-US03-21703-94 Sequence 94, Appl
33 76 11.8 287 7 US-60-487-610-2600 Sequence 58, Appl
34 76 11.8 287 7 US-60-485-450-1652 Sequence 1652, Ap
35 76 11.8 287 7 US-60-487-610-2600 Sequence 1652, Ap
36 74.5 11.5 335 1 PCT-US03-21703-102 Sequence 102, Appl
37 74.5 11.5 335 7 US-60-487-610-2601 Sequence 2601, Ap
38 74.5 11.5 335 7 US-60-485-450-1653 Sequence 1653, Ap
39 74.5 11.5 576 6 US-10-293-244-3820 Sequence 3820, Ap
40 74.5 11.5 576 6 US-10-293-244-3821 Sequence 3821, Ap
41 74.5 11.5 576 6 US-10-286-897-6863 Sequence 6863, Ap
42 74.5 11.5 576 6 US-10-258-898A-6863 Sequence 6863, Ap
43 74.5 11.5 603 6 US-10-293-244-1853 Sequence 1853, Ap
44 74.5 11.5 636 6 US-10-286-897-3291 Sequence 3291, Ap
45 74.5 11.5 636 6 US-10-258-898A-3291 Sequence 3291, Ap

ALIGNMENTS

RESULT 1

US-10-631-402-2576
; Sequence 2576, Application US/10631402
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; FILE REFERENCE: GEN-T119C1
; CURRENT APPLICATION NUMBER: US/10/631,402
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/547,599C
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 08/905,223
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,135
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,051
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,144
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,279
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/904,468
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,134
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: US 08/905,133
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 3475
; SOFTWARE: Patent.pm
; SEQ ID NO 2576
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Cancerous prostate
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -15...1
; OTHER INFORMATION: Von Heijne matrix
; FEATURE:
; OTHER INFORMATION: score 7.50
; FEATURE:
; OTHER INFORMATION: seq AVLLALLMAGLAL/QP
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Asp,His

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; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 16
; OTHER INFORMATION: Xaa = Gly,Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 12
; OTHER INFORMATION: Xaa = Lys,Arg
US-10-631-402-2576

Query Match      68.3%; Score 441; DB 6; Length 88;
Best Local Similarity 95.5%; Pred. No. 1.2e-42;
Matches 84; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCTQLGEOCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCTQLGEOCWTARIRAVGLLT 60

Oy 61 VISKCSLNCVDDSDQYVVGKKNITCCD 88
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RESULT 2
PCT-US02-29560A-346
; Sequence 2576, Application US/10631441
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; FILE REFERENCE: GEN-T119C1
; CURRENT FILING DATE: 2003-07-30
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/547,599C
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 08/905,223
; PRIOR FILING DATE: 1997-08-01
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; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 3475
; SOFTWARE: Patent.pm
; SEQ ID NO 2576
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Cancerous prostate
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -15..-1
; OTHER INFORMATION: Von Heijne matrix
; FEATURE:
; OTHER INFORMATION: score 7.50
; FEATURE:
; OTHER INFORMATION: seq AVLLALLMAGLAL/QP
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Asp,His
; FEATURE:
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; NAME/KEY: UNSURE
; LOCATION: 16
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; OTHER INFORMATION: Xaa = Lys,Arg
US-10-631-441-2576

Query Match      68.3%; Score 441; DB 6; Length 88;
Best Local Similarity 95.5%; Pred. No. 1.2e-42;
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Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCTQLGEOCWTARIRAVGLLT 60

Oy 61 VISKCSLNCVDDSDQYVVGKKNITCCD 88
Db 61 VISKCSLNCVDDSDQYVVGKKNITCCD 88

RESULT 3
PCT-US02-29560A-346
; Sequence 346, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT FILING DATE: 2002-09-17
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/323,469
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 346
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-346

Query Match      24.5%; Score 158.5; DB 1; Length 131;
Best Local Similarity 35.3%; Pred. No. 8.5e-11;
Matches 47; Conservative 18; Mismatches 53; Indels 15; Gaps 5;

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Db 1 MKIFLPVLLAALLGVERASSLMCFSCNLQKSNLYCLKPTICSDQDNYCVTVSASAGIGNL 60

Oy 60 TV---ISKGCSLNC-VDDSDQYVVGKKNITCCDIDLCKXSGAH-----ALQPAAIL 107
Db 61 VTFGHSLSKTCSPACPIPEGVNVGVASMGISCCQSFCLNFSADGGLRASVTLGAGILL 120

Oy 108 ALLPALGLLLWGP 120
Db 121 SLLPA--LLRFGP 131

RESULT 4
US-60-485-450-1070
; Sequence 1070, Application US/60485450
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CHANG, Sheng-yung
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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US-10-258-898A-2973

Query Match 19.9%; Score 128.5; DB 6; Length 116;
Best Local Similarity 30.0%; Pred. No. 1.7e-07;
Matches 36; Conservative 13; Mismatches 64; Indels 7; Gaps 3;
Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLLT 60
Db 1 MTPLLTLILVLMGLPLAQLDCHVC--AYGNDNCFNMRCPAMVAYCMTTRITYTPTRM 58
Qy 61 VISKGCSLNCVDDSDQYVVGKKNIT-CCDTDLCKXSGAHALQPAALILALLPALGLLWG 119
Db 59 KVKSCVPRCFETVYDGYGSKHASTTSCQYDLNCGTGL----ATPATLALAPILLATLWG 114

RESULT 8

US-10-286-897-6545
; Sequence 6545, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286.897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-897-6545

Query Match 19.9%; Score 128.5; DB 6; Length 128;
Best Local Similarity 30.0%; Pred. No. 1.9e-07;
Matches 36; Conservative 13; Mismatches 64; Indels 7; Gaps 3;
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RESULT 9

US-10-258-898A-6545
; Sequence 6545, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/258.898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317

; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6545
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-898A-6545

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Matches 36; Conservative 13; Mismatches 64; Indels 7; Gaps 3;
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Qy 61 VISKGCSLNCVDDSDQYVVGKKNIT-CCDTDLCKXSGAHALQPAALILALLPALGLLWG 119
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; Sequence 14, Application PC/TUS0318400
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals
; TITLE OF INVENTION: Cancer-Linked Gene as Target for Chemotherapy
; FILE REFERENCE: 689290-158
; CURRENT APPLICATION NUMBER: PCT/US03/18400
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US/60/388,157
; PRIOR FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-18400-14

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Qy 105 AILALLPALGL 115
Db 126 RTTILFLKIAL 136

RESULT 11

PCT-US02-29560A-322
; Sequence 322, Application PC/TUS0229560A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:43:44 ; Search time 54 Seconds
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298.396 Million cell updates/sec

Title: US-09-934-586A-2

Perfect score: 646

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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	645	99.8	123	10	US-09-855-153-6
5	645	99.8	123	10	US-09-854-811-2
6	645	99.8	123	10	US-09-854-811-6
7	645	99.8	123	10	US-09-934-773-2
8	645	99.8	123	10	US-09-934-773-6
9	645	99.8	123	10	US-09-963-620-2
10	645	99.8	123	10	US-09-963-620-6
11	645	99.8	123	11	US-09-855-632-2
12	645	99.8	123	11	US-09-855-632-6
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17	644	99.7	123	9	US-09-934-586A-2	Sequence 2, Appli
18	388	60.1	123	9	US-09-564-329A-7	Sequence 7, Appli
19	388	60.1	123	10	US-09-855-153-7	Sequence 7, Appli
20	388	60.1	123	10	US-09-854-811-7	Sequence 7, Appli
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35	158.5	24.5	131	9	US-09-564-329A-5	Sequence 5, Appli
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43	154.5	23.9	131	14	US-10-101-747-2	Sequence 2, Appli
44	153.5	23.8	131	9	US-09-934-586A-1	Sequence 1, Appli
45	144	22.3	136	9	US-09-934-586A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-564-329A-2
; Sequence 2, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Safran, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123

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; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-564-329A-2

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Best Local Similarity 99.2%; Pred. No. 1.1e-62;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 GOL 123
Db 121 GOL 123

RESULT 2
US-09-564-329A-6
; Sequence 6, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
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; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
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; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
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; LOCATION: (67)..(81)
US-09-564-329A-6

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Best Local Similarity 99.2%; Pred. No. 1.1e-62;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 121 GOL 123

RESULT 3
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; Sequence 2, Application US/09855153
; Patent No. US20020102666A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855,153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
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; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/855.153
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
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US-09-855-153-6

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RESULT 5
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; Sequence 2, Application US/09854811

; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854.811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
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; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
; NAME/KEY: SITE
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; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-854-811-2

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Best Local Similarity 99.2%; Pred. No. 1.le-62;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 121 GOL 123
Db 121 GOL 123

RESULT 6
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; Sequence 6, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854.811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-09-854-811-6

Query Match 99.8%; Score 645; DB 10; Length 123;
Best Local Similarity 99.2%; Pred. No. 1.le-62;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
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; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
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; SEQ ID NO 2
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US-09-963-620-2

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; Sequence 6, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
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; PRIOR APPLICATION NUMBER: 09/359,326
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; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
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; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/10/224,720
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; PRIOR FILING DATE: 1999-07-20
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; Publication No. US2003013820A1
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; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
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; PRIOR FILING DATE: 1999-07-20
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:39:59 ; Search time 29 Seconds
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Listing first 45 summaries

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ALIGNMENTS

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; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
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; APPLICANT: Witte, Robert E.
; APPLICANT: Reiter, Owen N.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203.939
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; APPLICANT: Witte, Robert E.
; APPLICANT: Reiter, Owen N.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN
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; APPLICANT: Witte, Robert E.
; APPLICANT: Reiter, Owen N.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
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; CURRENT FILING DATE: 1999-02-17
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; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318.503A
; EARLIER FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)..(81)
; US-09-318-503-2

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Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 121 GOL 123
Db 121 GOL 123

RESULT 6
US-09-318-503-6
; Sequence 6, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318.503A
; EARLIER FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
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; LOCATION: (71)..(82)
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; LOCATION: (67)..(81)
; US-09-318-503-2

Query Match          99.8%; Score 645; DB 3; Length 123;
Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60

Oy 61 VISKCSLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
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Oy 121 GOL 123
Db 121 GOL 123

RESULT 7
US-09-038-261A-2
; Sequence 2, Application US/09038261A
; Patent No. 6267960
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/038.261A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
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; LOCATION: (71)..(82)
; US-09-038-261A-2

Query Match          99.8%; Score 645; DB 3; Length 123;
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Oy 121 GOL 123
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; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
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; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; US-09-318-503-6

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Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 121 GOL 123
Db 121 GOL 123

RESULT 7
US-09-038-261A-2
; Sequence 2, Application US/09038261A
; Patent No. 6267960
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/038.261A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSKA (hPSCA)
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)..(64)
; NAME/KEY: SITE
; LOCATION: (71)..(82)
; US-09-038-261A-2

Query Match          99.8%; Score 645; DB 3; Length 123;
Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
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Oy 61 VISKCSLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
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Oy 121 GOL 123
Db 121 GOL 123
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-09-564-329A-6

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Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKNSGAHALQPAIAIALLPALGLLWGP 120
Qy 121 GOL 123
Db 121 GOL 123

RESULT 12
US-09-203-939-7
; Sequence 7, Application US/09203939
; Patent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US11
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: MURINE PSCA (mPSCA)
US-09-203-939-7

Query Match          60.1%; Score 388; DB 3; Length 123;
Best Local Similarity 58.5%; Pred. No. 6e-38;
Matches 72; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

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Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKNSGAHALQPAIAIALLPALGLLWGP 120
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RESULT 13
US-09-351-835-7
; Sequence 7, Application US/09251835A
; Patent No. 6261789
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54US12
; CURRENT APPLICATION NUMBER: US/09/251,835A
; CURRENT FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/038,261
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-09-564-329A-6

Query Match          99.8%; Score 645; DB 4; Length 123;
Best Local Similarity 99.2%; Pred. No. 5.1e-68;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKNSGAHALQPAIAIALLPALGLLWGP 120
Qy 121 GOL 123
Db 121 GOL 123

RESULT 11
US-08-675-508-2
; Sequence 2, Application US/08675508
; Patent No. 5856136
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,508
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0066 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: SCAH-2
; CLONE:
US-08-675-508-2

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; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: MURINE PSKA (mpSCA)
US-09-251-835-7

Query Match      60.1%; Score 388; DB 3; Length 123;
Best Local Similarity 58.5%; Pred. No. 6e-38;
Matches 72; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 7, Application US/09318503A
; Patent No. 6261791
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US13
; CURRENT APPLICATION NUMBER: US/09/318,503A
; CURRENT FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 08/814,279
; EARLIER FILING DATE: 1997-03-10
; EARLIER APPLICATION NUMBER: 60/071,141
; EARLIER FILING DATE: 1998-01-12
; EARLIER APPLICATION NUMBER: 60/074,675
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 09/038,261
; EARLIER FILING DATE: 1998-03-10
; EARLIER APPLICATION NUMBER: 09/203,939
; EARLIER FILING DATE: 1998-12-02
; EARLIER APPLICATION NUMBER: 09/251,835
; EARLIER FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 18
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; ORGANISM: MURINE PSKA (mpSCA)
US-09-318-503-7

Query Match      60.1%; Score 388; DB 3; Length 123;
Best Local Similarity 58.5%; Pred. No. 6e-38;
Matches 72; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

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; Patent No. 6267960
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; TITLE OF INVENTION: PSKA: PROSTATE STEM CELL ANTIGEN
; FILE REFERENCE: 30435.54USU1
; CURRENT APPLICATION NUMBER: US/09/038,261A
; CURRENT FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: MURINE PSKA (mpSCA)
US-09-038-261A-7

Query Match      60.1%; Score 388; DB 3; Length 123;
Best Local Similarity 58.5%; Pred. No. 6e-38;
Matches 72; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:31:29 ; Search time 85 Seconds
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Title: US-09-934-586a-2

Perfect score: 646

Sequence: 1 MKAVLLALLMAGLALQPGTA.....AAILALLPALGLLLMSPGQL 123

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Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	645	99.8	123	20	AAW86024 UT116 polypeptide
4	645	99.8	123	21	AAV99707 Human prostate ste
5	645	99.8	123	22	AAEQ3746 Human prostate ste
6	645	99.8	123	23	AAU76692 Human prostate ste
7	645	99.8	123	24	ABR48224 Human bladder canc
8	645	99.8	123	24	ABP74203 Human PSCA protein
9	644	99.7	125	19	AAW62066 Human stem cell an

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11	640	99.1	123	22	AAW35285 Human prostate ste
12	627	97.1	119	23	AAU86131 Human PRO232 polyp
13	607	94.0	114	20	AAV13347 Amino acid sequenc
14	600	92.9	123	22	AAE03759 Cynomolgus (monkey
15	594	92.0	123	22	AAE03758 Cynomolgus (monkey
16	441	68.3	88	20	AAV11900 Human 5' EST seque
17	441	68.3	88	21	AAU00606 Human secreted pro
18	388	60.1	123	21	AAV99711 Murine prostate ste
19	384	59.4	123	19	AAW30568 Murine prostate ste
20	384	59.4	123	21	AAV99708 Murine prostate ste
21	384	59.4	123	22	AAW35286 Murine prostate ste
22	384	59.4	123	23	AAU76693 Mouse prostate ste
23	276	42.7	117	22	ABW11977 Human stem cell Ag
24	268	41.5	85	23	ABP08688 Human ORFX protein
25	224	34.7	41	20	AAW80958 PS116 antigen. Ho
26	224	34.7	41	20	AAW86026 Peptide epitope 2
27	191	29.6	34	20	AAW80957 PS116 antigen. Ho
28	191	29.6	34	20	AAW86025 Peptide epitope 1
29	169	26.2	30	20	AAW80959 PS116 antigen. Ho
30	169	26.2	30	20	AAW86027 Peptide epitope 3
31	167.5	25.9	131	21	AAV99709 Human stem cell an
32	158.5	24.5	131	17	AAW83017 Haematopoietic ste
33	158.5	24.5	131	19	AAW69214 Osteoclast inhibit
34	155.5	24.1	131	22	AAW35287 Human stem cell an
35	154.5	23.9	131	18	AAW24847 Human stem cell an
36	154.5	23.9	131	21	AAW29923 Human stem cell an
37	154.5	23.9	131	23	ABG71306 Human stem cell an
38	153.5	23.8	131	19	AAW62065 Human stem cell an
39	143	22.1	138	21	AAW29924 Murine stem cell a
40	141.5	21.9	125	22	AAE03301 Human gene 10 enco
41	141.5	21.9	125	22	AAE03327 Human gene 10 enco
42	141.5	21.9	125	23	ABG64428 Human albumin fusi
43	141.5	21.9	125	23	ABG64430 Human albumin fusi
44	138.5	21.4	125	20	AAV41956 Human PRO788 prote
45	138.5	21.4	125	21	AAW44312 Human PRO788 (UNQ4

ALIGNMENTS

RESULT 1	AAW70522	AAW70522 standard; Protein; 123 AA.
ID	AAW70522	Protein; 123 AA.
XX	AC	AAW70522;
XX	DT	02-FEB-1999 (first entry)
XX	DE	Human prostate stem cell antigen (PSCA).
XX	KW	Prostate stem cell antigen; PSCA; human; prostate cancer;
XX	XX	diagnosis; therapy; vaccine; antibody.
XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	Peptide
XX	FT	Peptide
XX	XX	Location/Qualifiers
XX	XX	50..64
XX	XX	/note= "claimed fragment (Claim 5)"
XX	XX	71..82
XX	XX	/note= "claimed fragment (Claim 6)"
XX	XX	WO9840403-A1.
XX	XX	17-SEP-1998.
XX	XX	10-MAR-1998; 98WO-US04665.
XX	XX	13-FEB-1998; 98US-0074675.
XX	XX	10-MAR-1997; 97US-0814279.
XX	XX	12-JAN-1998; 98US-0071141.
XX	XX	(REGC) UNIV CALIFORNIA.
XX	XX	PA

XX Reiter R, Witte O;
 XX WPI; 1998-520601/44.
 DR N-PSDB; AAV33691.
 XX
 PT New prostate stem cell antigen protein, PSCA - useful in diagnosis
 PT and treatment of prostate cancer, e.g. to produce vaccines or
 PT generate antibodies for use in assays or therapeutically
 XX
 PS Claim 2; Fig 1B; 63pp; English.
 XX
 CC This polypeptide comprises a novel human prostate-specific cell
 CC surface antigen (PSCA) that is widely over-expressed across all
 CC stages of prostate cancer, including high grade prostate
 CC intraepithelial neoplasia and androgen-dependent and -independent
 CC prostate tumours. The amino acid sequence was deduced from
 CC isolated cDNA clones (see AAV33691), and contains the highly
 CC conserved cysteine residues of the Ly-6/Thy-1 gene family, as well
 CC as showing homology to GPI-anchored proteins. PSCA proteins may be
 CC used as diagnostic and/or prognostic markers of prostate cancer;
 CC PSCA (or encoding nucleic acids) can also be used therapeutically
 CC in vaccines, in assays to isolate ligands or other binding agents
 CC and to produce antibodies. PSCA antibodies are useful in
 CC diagnostic/prognostic assays to detect PSCA, e.g. to diagnose or
 CC monitor the progress of prostate cancer in subjects. Claimed
 CC immunoconjugates, including an antigen binding region (see
 CC AAW70523-24) of the antibody and a toxin agent such as ricin, can be
 CC used to selectively kill cells expressing PSCA antigens (claimed).
 CC Host vector systems and a method of producing PSCA protein are
 CC also claimed.
 XX
 SQ Sequence 123 AA;
 Query Match 99.8%; Score 645; DB 19; Length 123;
 Best Local Similarity 99.2%; Pred. No. 2.9e-63;
 Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
 Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
 Qy 121 GQL 123
 Db 121 GQL 123
 RESULT 2
 AAW80956
 ID AAW80956 standard; Prptein; 123 AA.
 XX
 AC AAW80956;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE PS116 antigen.
 XX
 KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO9851805-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US10041.
 XX
 PR 15-MAY-1997; 97US-0856653.

XX (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Kloss MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 1999-045234/04.
 XX
 PT New method for detecting diseases of the prostate - comprises use of
 PT a PS116 polynucleotide, protein or antibodies, useful for preventing
 PT and treating prostate infections and cancer
 XX
 PS Claim 17; Page 97; 118pp; English.
 XX
 CC This sequence represents a PS116 antigen. The PS116 gene sequences were
 CC isolated as expressed sequence tag (EST) clone of the PS116 gene isolated
 CC from a human prostate tissue library. The PS116 sequences can be used in
 CC the method of the invention for detecting a target PS116 polynucleotide
 CC (PN), that comprises: contacting a sample with at least 1 PS116-specific
 CC PN or complement; and detecting the target PS116 PN, where the specific
 CC PN has at least 50% identity with the PS116 sequences. The PN, PS116
 CC polypeptides (such as this sequence) or PS116 amplicons are used to
 CC detect prostate disease. Antibodies (Abs) against PS116 are used in assay
 CC kits to detect PS116 antigen or anti-PS116 Ab, and the Abs are preferably
 CC attached to a solid phase. The polypeptides are used for detecting
 CC PS116-specific Abs in a sample, and for producing Abs after immunising a
 CC subject. Plasmids encoding PS116 epitopes can also be administered to a
 CC subject to obtain Abs. The cDNAs and polypeptides are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
 CC imaging, preventing, treating or determining the predisposition of a
 CC cancer. The Abs and agonists or conditions of the prostate, such as prostate
 CC cancer. The Abs and agonists or inhibitors are useful for treating
 CC prostate diseases, tumours and metastases.
 XX
 SQ Sequence 123 AA;
 Query Match 99.8%; Score 645; DB 20; Length 123;
 Best Local Similarity 99.2%; Pred. No. 2.9e-63;
 Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
 Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDTDLCKNSGAHALQPAALAILALLPALGILLWGP 120
 Qy 121 GQL 123
 Db 121 GQL 123
 RESULT 3
 AAW86024
 ID AAW86024 standard; Protein; 123 AA.
 XX
 AC AAW86024;
 XX
 DT 23-FEB-1999 (first entry)
 XX
 DE UT116 polypeptide consensus sequence.
 XX
 KW UT116; urinary tract; epitope; antigen; detection; diagnosing;
 KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
 KW metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO9851824-A1.
 XX
 PR 19-NOV-1998.

```

XX 15-MAY-1998; 98WO-US09972.
XX 15-MAY-1997; 97US-0856652.
XX (ABBO ) ABBOTT LAB.
XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
XX Granaods EN, Hodges SC, Klass MR, Kratochvil JD;
XX Roberts-rapp L, Russell JC, Stroupe SD;
XX WPI: 1999-045237/04.
XX N-PSDB; AAV80396; AAV80397.
XX New method for detecting diseases of the urinary tract - comprises
XX use of a UT116 polynucleotide, protein or antibodies, used for
XX preventing and treating urinary tract infections and cancer
XX Claim 10; Page 94; 113pp; English.
XX This represents the consensus sequence of the UT116 polypeptide, derived
XX from urinary tract tissue. The invention relates to a method of
XX detecting the presence of a target UT116 polynucleotide in a test sample
XX using UT116 gene-specific sequences (AAV80386 to AAV80397). Host cells
XX transfected with an expression vector containing the UT116 gene can be
XX used to produce a UT116 polypeptide recombinantly. This polypeptide has
XX at least one UT116 epitope which can be used in a method for detecting
XX UT116 antigen in a test sample. The polynucleotides and polypeptides are
XX useful for detecting, diagnosing, monitoring, staging, prognosticating,
XX in vivo imaging, preventing, treating or determining the predisposition
XX of a subject to diseases and conditions of the urinary tract, such as
XX urinary tract cancer. Antibodies specifically binding to an epitope of
XX UT116 antigen, and agonists are useful for treating urinary tract
XX diseases, tumours and metastases.
XX Sequence 123 AA;
Query Match 99.8%; Score 645; DB 20; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.9e-63;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALPGTALLCYSCAKQVSNEDCLQVENCITQLGECQWTARIRAVGLLT 60.
Db 1 MKAVLLALLMAGLALPGTALLCYSCAKQVSNEDCLQVENCITQLGECQWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKXSGAHALQPAALAILLALPALGLLLWGP 120
Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKXSGAHALQPAALAILLALPALGLLLWGP 120
Qy 121 GQL 123
Db 121 GQL 123
RESULT 4
AAV99707
ID AAV99707 standard; Protein; 123 AA.
XX AAV99707;
AC AAV99707;
XX 07-SEP-2000 (first entry)
XX Human prostate stem cell antigen, PSCA.
XX Human; prostate cancer; prostate stem cell antigen; PSCA;
XX chromosome 8q24.2; bladder cancer; anti-apoptosis; proliferation;
XX GPI-anchored cell surface antigen; glycosylphosphatidylinositol.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= signal_peptide

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FT Misc-difference 1 /note= "Encoded by GTG"
FT Protein- 21..123 /label= Mature_protein
FT Modified-site 32 /note= "N-glycosylated"
FT Modified-site 40 /note= "N-glycosylated"
FT Misc-difference 74 /note= "Encoded by TTA"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 93 /note= "N-glycosylated"
FT Region 100..123 /label= GPI-anchoring_sequence
XX W0200032752-A1.
XX 08-JUN-2000.
XX 02-DEC-1999; 99WO-US28883.
XX 02-DEC-1998; 98US-0203939.
XX 17-FEB-1999; 99US-0251835.
XX 25-MAY-1999; 99US-0318503.
XX (REGC ) UNIV CALIFORNIA.
XX Reiter R, Witte O;
XX WPI: 2000-412305/35.
XX N-PSDB; AAA48374.
XX Prostate stem cell antigens, the nucleic acids encoding them and
XX antibodies against them, useful for diagnosing and treating prostate
XX cancer, bladder carcinomas and/or bone metastases of prostate cancer -
XX Claim 18; Fig 1; 171pp; English.
XX The present sequence is the human Prostate Stem Cell Antigen (PSCA).
XX PSCA is a glycosylphosphatidylinositol (GPI)-anchored cell surface
XX antigen, which is expressed across a variety of normal cells: prostate
XX cells, urothelium, renal collecting ducts, colonic neuroendocrine cells,
XX placenta, bladder and ureteral transitional epithelial cells. However,
XX PSCA is widely over-expressed across all stages of prostate cancer,
XX including high grade prostatic intraepithelial neoplasia (PIN),
XX androgen-dependent and androgen-independent prostate tumours and bladder
XX carcinoma. The expression of PSCA appears to correlate with increasing
XX grade and so PSCA may be used as a prostate cancer marker, to
XX discriminate between malignant prostate cancers, normal prostate glands
XX and non-malignant neoplasias. It is hypothesised that PSCA may play a
XX role in stem/progenitor cell function such as self-renewal
XX (anti-apoptosis) and/ or proliferation. The PSCA gene has been localised
XX to chromosome 8q24.2. Fragments of the present sequence (AAV99712,
XX AAV99713 and AAV99714) may be used as antigens to produce antibodies
XX against PSCA. The antibodies may then be used to detect and quantify the
XX presence of PSCA proteins in samples and hence diagnose and prognose
XX prostate cancer. The antibodies may also be used in the treatment of
XX cancers associated with PSCA by inhibiting its expression.
XX Sequence 123 AA;
Query Match 99.8%; Score 645; DB 21; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.9e-63;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALPGTALLCYSCAKQVSNEDCLQVENCITQLGECQWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALPGTALLCYSCAKQVSNEDCLQVENCITQLGECQWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLCKXSGAHALQPAALAILLALPALGLLLWGP 120

```

Db 61 VISKCSLNCVDDSDQYYVVGKKNITCCDTDLCSAGAHALQPAIAAILALLPALGLLLWGP 120

Qy 121 GOL 123
|||

Db 121 GOL 123

RESULT 5

AAE03746
ID AAE03746 standard; Protein; 123 AA.

XX AAE03746;

DT 07-AUG-2001 (first entry)

XX Human prostate stem cell antigen (PSCA) protein.

XX Human; prostate stem cell antigen; PSCA; cytostatic; gene therapy;

KW glycoprotein; cancer; prostate; bladder; lung; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20

FT /label= Signal_peptide

FT Protein 21..123

FT /label= Mature_human_PSCA_protein

FT Region 21..100

FT /note= "C-terminal GPI-anchoring sequence"

XX WO200140309-A2.

XX 07-JUN-2001.

XX 27-OCT-2000; 2000WO-US29603.

XX 29-OCT-1999; 99US-0162558.

PR 16-FEB-2000; 2000US-0182872.

XX (GETH) GENENTECH INC.

XX Devaux B, Keller G, Koeppen H, Lasky LA;

XX WPI; 2001-389954/41.

XX N-PSDB; AAD08171.

XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes

FT on binding to PSCA on mammalian cell and inhibits growth of

PT PSCA-expressing cancer cells in vivo, useful for killing

PT PSCA-expressing cancer cells -

XX Example 1; Fig 17; 112pp; English.

XX The present sequence is human prostate stem cell antigen (PSCA).

CC PSCA is a single subunit glycoprotein that is expressed on the

CC cell surface as a glycosylphosphatidylinositol (GPI)-anchored

CC protein. The present invention relates to anti-PSCA antibody composition

CC and methods of killing PSCA-expressing cancer cells. PSCA is useful for

CC inhibiting and killing the growth of PSCA-expressing cancer cells such as

CC prostate cancer, bladder cancer or lung cancer cells. Humanised antibody

CC conjugated to a toxin or a radioactive isotope is used for killing the

CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing

CC tumour cells in vivo and for inhibiting or killing these cells. The

CC antibodies are also useful for treating the above mentioned cancers and

CC for diagnosing and staging of PSCA-expressing cancer, for purification

CC or immunoprecipitation of PSCA from cells, and for detection and

CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating

CC cancers by gene therapy techniques.

XX Sequence 123 AA;

Query Match 99.8%; Score 645; DB 22; Length 123;

Best Local Similarity 99.2%; Pred. No. 2.9e-63;

Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQGTALLCYSCKAQVSNEDCLOVENCQTOLGEOCWTARIRAVGLLT 60
|||||

Db 1 MKAVLLALLMAGLALQGTALLCYSCKAQVSNEDCLOVENCQTOLGEOCWTARIRAVGLLT 60
|||||

Qy 61 VISKCSLNCVDDSDQYYVVGKKNITCCDTDLCSAGAHALQPAIAAILALLPALGLLLWGP 120
|||||

Db 61 VISKCSLNCVDDSDQYYVVGKKNITCCDTDLCSAGAHALQPAIAAILALLPALGLLLWGP 120
|||||

Qy 121 GOL 123
|||

Db 121 GOL 123

RESULT 6

AAU76692
ID AAU76692 standard; Protein; 123 AA.

XX AAU76692;

XX 21-MAY-2002 (first entry)

DT Human prostate stem cell antigen (PSCA) protein sequence.

XX Human; prostate stem cell antigen; PSCA; antibody; immunogen;

KW prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;

FT PSCA-associated cancer; PSCA antigen.

XX Homo sapiens.

OS US2001055751-A1.

XX 27-DEC-2001.

XX 03-MAY-2000; 2000US-0564329.

XX 10-MAR-1997; 97US-228816P.

PR 12-JAN-1998; 98US-071141P.

PR 13-FEB-1998; 98US-074675P.

PR 21-DEC-1998; 98US-113210P.

PR 17-FEB-1999; 99US-120536P.

PR 16-MAR-1999; 99US-124658P.

PR 10-MAR-1998; 98US-0038261.

PR 02-DEC-1998; 98US-0203939.

PR 17-FEB-1999; 99US-0251835.

PR 25-MAY-1999; 99US-0318503.

PR 20-JUL-1999; 99US-0359326.

XX (REIT/) REITER R E.

PA (WITT/) WITTE O N.

PA (SAFF/) SAFFRAN D C.

PA (JAKO/) JAKOBOVITS A.

XX Reiter RE, Witte ON, Safran DC, Jakobovits A;

XX WPI; 2002-194864/25.

DR N-PSDB; ABK09980.

XX New antibodies specifically binding a novel prostate cell surface

PT antigen, PSCA, useful as antitumour agents in treatment of prostate,

FT bladder and pancreatic cancer and in prostate cancer diagnosis -

XX Example 1; Fig 1b; 127pp; English.

XX The present invention relates to new antibodies that specifically bind a

CC novel prostate stem cell antigen (PSCA), which is widely over-expressed

CC across all stages of prostate cancer. The antibodies of the invention

CC are useful to kill tumour cells expressing PSCA and as PSCA expression is

CC observed in prostate tumour cells and in other human cancers,

CC particularly bladder and pancreatic carcinomas, the antibodies are

CC useful therapeutically to treat these diseases. In particular, monoclonal

CC antibodies can be administered to subjects suffering from PSCA-associated

CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic
 CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong
 CC the subject's life. The antibodies can be combined with a therapeutic
 CC agent in immunoconjugates useful to treat subjects suffering from
 CC malignant diseases, characterised by cells having PSA antigen on the
 CC cell surface e.g. cancers, by killing the cells. The antibodies and
 CC immunoconjugates may also be included with a carrier in pharmaceutical
 CC compositions useful to kill human cells expressing PSA antigen on the
 CC cell surface. The antibodies are also useful diagnostically to detect
 CC cancers, especially prostate cancer, to isolate prostate cancer cells
 CC e.g. to enable culture growth to evaluate candidate therapeutic
 CC compounds, assist in identification of rare genes associated with
 CC prostate cancer, and to isolate and purify PSA and PSA homologues.
 CC The present amino acid sequence represents the human prostate stem cell
 CC antigen (PSCA) protein of the invention.

XX Sequence 123 AA;

Query Match 99.8%; Score 645; DB 23; Length 123;
 Best Local Similarity 99.2%; Pred. No. 2.9e-63;
 Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 DB 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 QY 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLXNSGAHALQPAALALLPALGLLLWGP 120
 DB 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLXNSGAHALQPAALALLPALGLLLWGP 120
 QY 121 GQL 123
 DB 121 GQL 123

RESULT 7

ABR48224
 ID ABR48224 standard; Protein; 123 AA.

XX ABR48224;

DT 12-JUN-2003 (first entry)

DE Human bladder cancer associated protein sequence SEQ ID NO:169.

XX Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO2003003906-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US21338.

XX 03-JUL-2001; 2001US-302814P.

XX 03-AUG-2001; 2001US-310099P.

XX 08-NOV-2001; 2001US-343705P.

XX 13-NOV-2001; 2001US-350666P.

XX 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Mack DH, Aziz N;

XX WPI; 2003-201532/19.

XX N-PSDB; ACC51040.

PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with
 PT a bladder cancer-associated polynucleotide or antibody -

XX Claim 10; Page 288; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications.

XX Sequence 123 AA;

Query Match 99.8%; Score 645; DB 24; Length 123;
 Best Local Similarity 99.2%; Pred. No. 2.9e-63;
 Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 DB 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLOVENCQTQGEQCWTARIRAVGLLT 60
 QY 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLXNSGAHALQPAALALLPALGLLLWGP 120
 DB 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLXNSGAHALQPAALALLPALGLLLWGP 120
 QY 121 GQL 123
 DB 121 GQL 123

RESULT 8

ABP74203
 ID ABP74203 standard; Protein; 123 AA.

XX ABP74203;

DT 03-FEB-2003 (first entry)

DE Human PSCA protein SEQ ID NO:79.

XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 XX T cell.

XX Homo sapiens.

XX WO200281646-A2.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-US11101.

XX 06-APR-2001; 2001US-282211P.

XX 07-NOV-2001; 2001US-337017P.

XX 07-MAR-2002; 2002US-363210P.

XX (CTLI-) CTL IMMUNOTHERAPIES CORP.

XX Simard JUL, Diamond DC, Liu L, Xie Z;

XX WPI; 2003-067518/06.

XX N-PSDB; ABQ83853.

PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 PT encoding the peptides, that are useful epitopes of target-associated
 PT antigens -

XX Claim 1; Page 164; 352pp; English.

XX The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). AB083843 to AB083858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention.

XX SQ Sequence 123 AA;
Query Match 99.8%; Score 645; DB 24; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.9e-63;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCQTGECQWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCQTGECQWTARIRAVGLLT 60

Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALALLPALGILLWGP 120
Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALALLPALGILLWGP 120

Qy 121 GQL 123
Db 121 GQL 123

RESULT 9
AAW62066
ID AAW62066 standard; Protein; 125 AA.
XX AC AAW62066;
XX DT 14-SEP-1998 (first entry)
XX DE Human stem cell antigen 2.
XX KW Human; stem cell antigen; SCAH-1; SCAH-2; THP-1; bladder tumour;
XX KW diagnosis; screening; sca-2; LY-6 family; leukaemia; cancer.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 3..125
XX FT /label= SCAH-2
XX FT Misc-difference 96
XX FT /label= unknown
XX FT /note= "encoded by GSC"
XX FN WO9800540-A1.
XX PD 08-JAN-1998.
XX PF 25-JUN-1997; 97WO-US10956.
XX PR 03-JUL-1996; 96US-0675508.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Au-Young J;
XX DR WPI; 1998-427478/36.
XX DR N-PSDB; AAW38045.

PT Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g.
PT diagnose and treat SCAH-1 or SCAH-2 related conditions such as
PS tumours and screen inhibitory compounds
XX Claim 16; Fig 2; 65pp; English.

XX The present sequence represents human stem cell antigen 2 (SCAH-2). SCAH
CC proteins can be administered therapeutically, e.g. to inhibit or reverse
CC the development of tumours. Antibodies to SCAH proteins can be used in
CC diagnostic tests for conditions associated with protein expression in
CC biological samples, by combining a sample with the antibody under
CC conditions suitable for antibody binding to the protein to form a
CC complex, and detecting the complex. Antibodies to SCAH-2 are especially
CC useful in diagnostic tests for conditions/diseases such as leukaemias or
CC malignant local tumours associated with SCAH-2 expression. SCAH-1 and
CC SCAH-2 have homology to sca-2 and other stem cell antigens, and have
CC characteristics of the LY-6 family of cysteine rich proteins. The
CC functional similarities among LY-6 family proteins previously reported,
CC and the expression of SCAH-1 and SCAH-2 in tumours from several tissues
CC (e.g. breast, lung, bladder) indicated that SCAH proteins may be useful
CC as anticancer agents; SCAH antibodies, antagonists or inhibitors
CC identified using the proteins could also be useful in anticancer
CC treatments and to intervene in alloresponses associated with transplant
CC rejection and autoimmune diseases e.g. lupus nephritis. The nucleic acid
CC sequences encoding SCAH proteins are also useful therapeutically to
CC treat, e.g. leukaemias and cancers of the bladder or breast.

XX SQ Sequence 125 AA;
Query Match 99.7%; Score 644; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 3.8e-63;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCQTGECQWTARIRAVGLLT 60
Db 3 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCQTGECQWTARIRAVGLLT 62

Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALALLPALGILLWGP 120
Db 63 VISKGSCLNCVDDSDQYVVGKKNITCCDTDLCKNSGAHALQPAALALLPALGILLWGP 122

Qy 121 GQL 123
Db 123 GQL 125

RESULT 10
AAV13938
ID AAV13938 standard; Protein; 123 AA.
XX AC AAV13938;
XX DT 14-JUL-1999 (first entry)
XX DE Human transmembrane protein, HP01244.
XX KW Transmembrane protein; human; cell membrane; proliferation; diagnosis;
XX KW cell differentiation; carcinostatic agent; probe; gene therapy;
XX KW signal transduction; apoptosis; inhibitor;
XX KW phosphatidylethanolamine N-methyltransferase.
XX OS Homo sapiens.
XX PN W09918203-A2.
XX PD 15-APR-1999.
XX PF 05-OCT-1998; 98WO-JP04475.
XX PR 08-OCT-1997; 97JP-0276271.
XX PA (PROT-) PROTEGENE INC.
XX PA (SAGA) SAGAMI CHEM RES CENT.

XX Kato S, Kobayashi M, Sekine S, Yamaguchi T;
 XX WPI; 1999-277268/23.
 DR N-PSDB; AAX36800, AAX36801.
 XX Human transmembrane proteins and nucleotide sequences
 PT Claim 1; Page 82-83; 139pp; English.
 XX
 XX This sequence is a human transmembrane protein of the invention.
 CC All of the proteins exist in the cell membrane, so are considered to be
 CC proteins controlling the proliferation and differentiation of the cells.
 CC They may be useful as carcinostatic agents or as antigens for preparing
 CC antibodies against the proteins. The cDNAs can be used as probes for
 CC gene diagnosis and gene sources for gene therapy, as well as for
 CC large-scale expression of the proteins. The H901498 (see AAY13939)
 CC protein may be associated with signal transduction associated with
 CC apoptosis, and therefore useful in inhibition of apoptosis. The H901962
 CC (see AAY13943) protein can be used to treat diseases associated with
 CC phosphatidylethanolamine N-methyltransferase. The proteins are
 CC identified by the presence of a hydrophobic transmembrane region,
 CC knowledge of the protein function is not required, as in e.g. methods of
 CC expression cloning.
 XX
 SQ Sequence 123 AA;
 Query Match 99.2%; Score 641; DB 20; Length 123;
 Best Local Similarity 98.4%; Pred. No. 8.1e-63;
 Matches 121; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVNCITQLGECQWTARIRAVGLLT 60
 DB 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVNCITQLGECQWTARIRAVGLLT 60
 QY 61 VISKGSCLNCVDDSDQYVYVGGKNTCCDITLCNKXGAHALQPAALALLPALGLLLWGP 120
 DB 61 VISKGSCLNCVDDSDQYVYVGGKNTCCDITLCNKXGAHALQPAALALLPALGLLLWGP 120
 QY 121 GOL 123
 DB 121 GOL 123
 RESULT 11
 AAB35285
 ID AAB35285 standard; Protein; 123 AA.
 AC AAB35285;
 XX 08-MAY-2001 (first entry)
 XX Human prostate stem cell antigen.
 DE Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
 KW diagnosis; treatment; chromosome 8q24.2.
 XX Homo sapiens.
 OS
 XX WO200105427-A1.
 XX 25-JAN-2001.
 XX 20-JUL-2000; 2000WO-US19967.
 XX 20-JUL-1999; 99US-0359326.
 PR 03-MAY-2000; 2000US-0564329.
 XX (REGC) UNIV CALIFORNIA.
 PA (UROG-) UROGENESYS.
 XX
 PI Reiter R, Witte O, Saffran DC, Jakobovits A;
 XX
 WPI; 2001-159478/16.
 DR N-PSDB; AAF27971.
 XX
 PT Antibodies binding to prostate stem cell antigen inhibit the growth of
 DR cancer cells and are used to detect and treat prostate, pancreatic or
 PT bladder cancers -
 XX
 XX Example 1; Fig 1B; 229pp; English.
 XX
 CC The present invention describes a method of treating cancer associated
 CC with prostate stem cell antigen (PSCA) by administering an antibody which
 CC selectively binds to PSCA and inhibits the growth of the cancer cells.
 CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
 CC the human and murine PSCA protein and coding sequences, which can be used
 CC not only in the treatment of, but also in detection and prognosis of
 CC prostate cancer.
 XX
 SQ Sequence 123 AA;
 Query Match 99.1%; Score 640; DB 22; Length 123;
 Best Local Similarity 98.4%; Pred. No. 1e-62;
 Matches 121; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVNCITQLGECQWTARIRAVGLLT 60
 DB 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVNCITQLGECQWTARIRAVGLLT 60
 QY 61 VISKGSCLNCVDDSDQYVYVGGKNTCCDITLCNKXGAHALQPAALALLPALGLLLWGP 120
 DB 61 VISKGSCLNCVDDSDQYVYVGGKNTCCDITLCNKXGAHALQPAALALLPALGLLLWGP 120
 QY 121 GOL 123
 DB 121 GOL 123
 RESULT 12
 AAU86131
 ID AAU86131 standard; Protein; 119 AA.
 AC AAU86131;
 XX 15-JUL-2002 (first entry)
 XX Human PRO232 polypeptide.
 DE Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder;
 KW cytostatic; neuroprotective.
 XX Homo sapiens.
 OS
 XX WO200153486-A1.
 XX 26-JUL-2001.
 XX 11-FEB-2000; 2000WO-US03565.
 XX 08-MAR-1999; 99WO-US05028.
 PR 11-MAR-1999; 99US-123972P.
 PR 11-MAY-1999; 99US-133459P.
 PR 02-JUN-1999; 99WO-US12252.
 PR 22-JUN-1999; 99US-140650P.
 PR 22-JUN-1999; 99US-140653P.
 PR 20-JUL-1999; 99US-144758P.
 PR 26-JUL-1999; 99US-145698P.
 PR 28-JUL-1999; 99US-146222P.
 PR 17-AUG-1999; 99US-149395P.
 PR 31-AUG-1999; 99US-151689P.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
FA Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
PI Masters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
PI Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
DR N-PSDB; ABK40257.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for
PT treating benign or malignant tumours, leukaemias and lymphoid
PT malignancies, inflammatory, angiogenic and immunologic disorders -
XX Claim 61; Fig 8; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides and the polynucleotide sequences encoding them. The
CC PRO polypeptides, agonists, antagonists or anti-PRO antibodies are
CC useful for treating benign or malignant tumours (e.g. renal, kidney,
CC bladder, breast, etc), leukaemias and lymphoid malignancies, other
CC disorders such as neuronal, glial, astrocytal, hypothalamic, glandular,
CC macrophagal, stromal and blastocoeleic disorders, inflammatory, immune
CC and angiogenic disorders. The polynucleotide sequences are also
CC useful in gene therapy. AAU86128-AAU86162 represent the human PRO
CC polypeptides of the invention.
XX
XX Sequence 119 AA;
SQ
Query Match 97.1%; Score 627; DB 23; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.7e-61;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 LLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCCTQLGECQWTARIRAVGLLTWISK 64
Dy 1 LLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCCTQLGECQWTARIRAVGLLTWISK 60
Qy 65 GCSLNCVDDSDQYVYKKNITCCDTDLCKNSGAHALQPAAILLALLPALGLLWPGQL 123
Dy 61 GCSLNCVDDSDQYVYKKNITCCDTDLCKNSGAHALQPAAILLALLPALGLLWPGQL 119
RESULT 13
AA13347
ID AA13347 standard; Protein; 114 AA.
XX
XX AA13347;
XX
XX 25-JUN-1999 (first entry)
XX
XX Amino acid sequence of protein PRO232.
DE
XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
XX fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
XX anti-thrombotic; wound healing; tissue repair.
XX
XX Homo sapiens.
XX
XX WO9914328-A2.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-US19330.
XX
XX 25-NOV-1997; 97US-0066840.
PR 17-SEP-1997; 97US-0059113.

PR 17-SEP-1997; 97US-0059115.
PR 17-SEP-1997; 97US-0059117.
PR 17-SEP-1997; 97US-0059119.
PR 17-SEP-1997; 97US-0059121.
PR 17-SEP-1997; 97US-0059122.
PR 17-SEP-1997; 97US-0059184.
PR 18-SEP-1997; 97US-0059263.
PR 18-SEP-1997; 97US-0059266.
PR 15-OCT-1997; 97US-0062125.
PR 17-OCT-1997; 97US-0062285.
PR 17-OCT-1997; 97US-0062287.
PR 21-OCT-1997; 97US-0063486.
PR 24-OCT-1997; 97US-0062814.
PR 24-OCT-1997; 97US-0062816.
PR 24-OCT-1997; 97US-0063045.
PR 24-OCT-1997; 97US-0063120.
PR 24-OCT-1997; 97US-0063121.
PR 24-OCT-1997; 97US-0063127.
PR 24-OCT-1997; 97US-0063128.
PR 27-OCT-1997; 97US-0063329.
PR 27-OCT-1997; 97US-0063327.
PR 28-OCT-1997; 97US-0063541.
PR 28-OCT-1997; 97US-0063542.
PR 28-OCT-1997; 97US-0063544.
PR 28-OCT-1997; 97US-0063549.
PR 28-OCT-1997; 97US-0063550.
PR 28-OCT-1997; 97US-0063564.
PR 29-OCT-1997; 97US-0063435.
PR 29-OCT-1997; 97US-0063704.
PR 29-OCT-1997; 97US-0063732.
PR 29-OCT-1997; 97US-0063738.
PR 29-OCT-1997; 97US-0063734.
PR 29-OCT-1997; 97US-0064215.
PR 29-OCT-1997; 97US-0063735.
PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.

(GETH) GENENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.

N-PSDB; AAX52217.

New isolated human genes and polypeptides used in, e.g. treatment of
gastrointestinal ulceration

Claim 12; Fig 9; 320pp; English.

AA13344-403 represent secreted and transmembrane human proteins.
The cDNA sequences are obtained from cDNA libraries, prepared from
fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
The encoded polypeptides have specific uses based on their homology to
known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
associated with the preservation and maintenance of gastrointestinal
mucosa and the repair of acute and chronic mucosal lesions
(e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
ulceration and congenital microvillus atrophy), skin diseases associated
with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
cancers such as lung squamous cell carcinoma of the vulva and gliomas),
potent effects on cell growth and development, diseases related to

CC growth or survival of nerve cells including Parkinson's disease,
 CC Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
 CC for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used
 CC as a target for anti-tumor drugs. PRO533 may be used in the treatment
 CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have
 CC therapeutic applications in wound healing and tissue repair; PRO317 can
 CC be used for treating problems of the kidney, uterus, endometrium, blood
 CC vessels, or related tissue, e.g. in the heart of genital tract.

XX SQ Sequence 114 AA;
 Query Match 94.0%; Score 607; DB 20; Length 114;
 Best Local Similarity 99.1%; Pred. No. 4.1e-59;
 Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 MAGLALPGTALLCYCKAQVSNEDCLQVENCQTGECWTARIRAVGLLTIVISKGSLN 69
 Db |||||
 Qy 1 MAGLALPGTALLCYCKAQVSNEDCLQVENCQTGECWTARIRAVGLLTIVISKGSLN 60
 Db |||||
 Qy 70 CVDDSDQYVVGKKNITCCDITLCKNSGAHALQPAALILALLPALGLLLWPGQL 123
 Db |||||
 Qy 61 CVDDSDQYVVGKKNITCCDITLCKNSGAHALQPAALILALLPALGLLLWPGQL 114

RESULT 14
 AAE03759
 ID AAE03759 standard; Protein; 123 AA.

XX AC AAE03759;

XX DT 07-AUG-2001 (first entry)

XX DE Cynomolgus (monkey) type II prostate stem cell antigen (PSCA) protein.

XX KW Monkey; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 XX KW glycoprotein; cancer; prostate; bladder; lung; tumour.

XX OS Macaca fascicularis.

XX FH Key Location/Qualifiers

FT Peptide 1..20 /label= Signal_peptide

FT Protein 21..123

FT FT /label= Mature_typeII_PSCA_protein

FT Region 21..100

FT /note= "C-terminal GPI-anchoring sequence"

XX FN WO200140309-A2.

XX PD 07-JUN-2001.

XX PF 27-OCT-2000; 2000WO-US29603.

XX PR 29-OCT-1999; 99US-0162558.

XX PR 16-FEB-2000; 2000US-0182872.

XX PA (GETH) GENENTECH INC.

XX PI Devaux B, Keller G, Koeppen H, Lasky LA;

XX DR WPI; 2001-389954/41.

XX DR N-PSDB; AAD08175.

XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
 PT on binding to PSCA on mammalian cell and inhibits growth of
 PT PSCA-expressing cancer cells in vivo, useful for killing
 PT PSCA-expressing cancer cells -

XX PS Example 6; Fig 16; 112pp; English.

XX The present sequence is cynomolgus (monkey) type II prostate stem cell
 CC antigen (PSCA). PSCA is a single subunit glycoprotein that is expressed

CC on the cell surface as a glycosylphosphatidylinositol (GPI)-anchored
 CC protein. The present invention relates to anti-PSCA antibody composition
 CC and methods of killing PSCA-expressing cancer cells. PSCA is useful for
 CC inhibiting and killing the growth of PSCA-expressing cancer cells such as
 CC prostate cancer, bladder cancer or lung cancer cells. Humanised antibody
 CC conjugated to a toxin or a radioactive isotope is used for killing the
 CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing
 CC tumour cells in vivo and for inhibiting or killing these cells. The
 CC antibodies are also useful for treating the above mentioned cancers and
 CC for diagnosing and staging of PSCA-expressing cancer, for purification
 CC or immunoprecipitation of PSCA from cells, and for detection and
 CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
 CC cancers by gene therapy techniques.

XX SQ Sequence 123 AA;

Query Match 92.9%; Score 600; DB 22; Length 123;
 Best Local Similarity 93.5%; Pred. No. 2.7e-58;
 Matches 115; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALPGTALLCYCKAQVSNEDCLQVENCQTGECWTARIRAVGLLT 60

Db 1 MKAVLLALLMAGLALPGTALLCYCKAQVSNEDCLQVENCQTGECWTARIRAVGLLT 60

Qy 61 VISKGCNLCVDDSDQYVVGKKNITCCDITLCKNSGAHALQPAALILALLPALGLLLWGP 120

Db 61 VISKGCNLCVDDSDQYVVGKKNITCCDITLCKNSGAHALQPAALILALLPALGLLLWGP 120

Qy 121 GOL 123

Db 121 RQL 123

RESULT 15

AAE03758

ID AAE03758 standard; Protein; 123 AA.

XX AC AAE03758;

XX DT 07-AUG-2001 (first entry)

XX DE Cynomolgus (monkey) type I prostate stem cell antigen (PSCA) protein.

XX KW Monkey; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 XX KW glycoprotein; cancer; prostate; bladder; lung; tumour.

XX OS Macaca fascicularis.

XX FH Key Location/Qualifiers

FT Peptide 1..20 /label= Signal_peptide

FT Protein 21..123

FT /label= Mature_typeI_PSCA_protein

FT Region 21..100

FT /note= "C-terminal GPI-anchoring sequence"

XX FN WO200140309-A2.

XX PD 07-JUN-2001.

XX PF 27-OCT-2000; 2000WO-US29603.

XX PR 29-OCT-1999; 99US-0162558.

XX PR 16-FEB-2000; 2000US-0182872.

XX PA (GETH) GENENTECH INC.

XX PI Devaux B, Keller G, Koeppen H, Lasky LA;

XX DR WPI; 2001-389954/41.

XX DR N-PSDB; AAD08175.

XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes

PT on binding to PSCA on mammalian cell and inhibits growth of
PT PSCA-expressing cancer cells in vivo, useful for killing
PT PSCA-expressing cancer cells

XX Example 6; Fig 15; 112pp; English.

XX The present sequence is cynomolgus (monkey) type I prostate stem cell
CC antigen (PSCA). PSCA is a single subunit glycoprotein that is expressed
CC on the cell surface as a glycosylphosphatidylinositol (GPI)-anchored
CC protein. The present invention relates to anti-PSCA antibody composition
CC and methods of killing PSCA-expressing cancer cells. PSCA is useful for
CC inhibiting and killing the growth of PSCA-expressing cancer cells such as
CC prostate cancer, bladder cancer or lung cancer cells. Humanised antibody
CC conjugated to a toxin or a radioactive isotope is used for killing the
CC cancer cells. PSCA is useful for specifically targetting PSCA-expressing
CC tumour cells in vivo and for inhibiting or killing these cells. The
CC antibodies are also useful for treating the above mentioned cancers and
CC for diagnosing and staging of PSCA-expressing cancer, for purification
CC or immunoprecipitation of PSCA from cells, and for detection and
CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC cancers by gene therapy techniques.

XX SQ Sequence 123 AA;

Query Match 92.0%; Score 594; DB 22; Length 123;
Best Local Similarity 92.7%; Pred. No. 1.2e-57;
Matches 114; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCITGLGQCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCITGLGQCWTARIRAVGLLT 60
Qy 61 VISKGSILNCVDDSDQYVVGKKNITCCDTDLCKXGAHALQPAALALLPGLLLWGP 120
Db 61 VISKGSILNCVDDSDQYVVGKKNITCCDTDLCKXGAHALQPAALALLPGLLLWGP 120
Qy 121 QQL 123
Db 121 RQL 123

Search completed: August 18, 2003, 19:41:26
Job time : 86 secs

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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:44:29 ; Search time 84 Seconds
(without alignments)
232.421 Million cell updates/sec

Title: US-09-934-586A-2

Perfect score: 123

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	99.2	125	19 AAW62066	Human stem cell an
2	93	75.6	123	19 AAW70522	Human prostate ste
3	93	75.6	123	20 AAW80956	PS116 antigen. Ho
4	93	75.6	123	20 AAW86024	UT116 polypeptide
5	93	75.6	123	21 AAY95707	Human prostate ste
6	93	75.6	123	21 AAE03746	Human prostate ste
7	93	75.6	123	23 AAU76692	Human prostate ste
8	93	75.6	123	24 ABR48224	Human bladder can
9	93	75.6	123	24 ABP74203	Human PSCA protein

10	91	74.0	123	22 AAB35285	Human prostate ste
11	89	72.4	119	23 AAU86131	Human PRO332 poly
12	84	68.3	114	20 AAY13347	Amino acid sequenc
13	54	43.9	123	20 AAY13938	Human transmembran
14	51	41.5	117	22 ABE11977	Human stem cell Ag
15	41	33.3	41	20 AAW80958	PS116 antigen. Ho
16	41	33.3	41	20 AAW86026	Peptide epitope 2
17	41	33.3	88	20 AAY11900	Human 5' EST secre
18	41	33.3	88	21 AAG00606	Human secreted pro
19	36	29.3	123	22 AAE03758	Cynomolgus (monkey
20	36	29.3	123	22 AAE03759	Cynomolgus (monkey
21	34	27.6	34	20 AAW80957	PS116 antigen. Ho
22	34	27.6	34	20 AAW86025	Peptide epitope 1
23	24	19.5	24	20 AAW80960	PS116 antigen. Ho
24	24	19.5	24	20 AAW86028	Peptide epitope 4
25	24	19.5	30	20 AAW80959	PS116 antigen. Ho
26	24	19.5	30	20 AAW86027	Peptide epitope 3
27	15	12.2	15	19 AAW70523	Human prostate ste
28	15	12.2	15	21 AAY99712	Human prostate ste
29	15	12.2	15	21 AAY99714	Human prostate ste
30	15	12.2	15	22 AAB35282	Prostate stem cell
31	15	12.2	15	22 AAB35284	Prostate stem cell
32	12	9.8	12	19 AAW70524	Human prostate ste
33	12	9.8	12	21 AAY99713	Human prostate ste
34	12	9.8	12	22 AAB35283	Prostate stem cell
35	11	8.9	85	23 ABP08688	Human ORFX protein
36	10	8.1	10	24 ABP74340	Human PSCA epitope
37	10	8.1	10	24 ABP74342	Human PSCA epitope
38	9	7.3	9	24 ABP74339	Human PSCA epitope
39	9	7.3	9	24 ABP74341	Human PSCA epitope
40	8	6.5	8	24 ABP74338	Mouse prostate ste
41	8	6.5	123	19 AAW30568	Human prostate ste
42	8	6.5	123	21 AAY99708	Murine prostate st
43	8	6.5	123	21 AAY99711	Murine prostate st
44	8	6.5	123	22 AAB35286	Murine prostate st
45	8	6.5	123	23 AAU76693	Mouse prostate ste

ALIGNMENTS

RESULT 1

AAW62066

ID AAW62066 standard; Protein; 125 AA.

XX AC AAW62066;

XX DT 14-SEP-1998 (first entry)

XX DE Human stem cell antigen 2.

XX KW Human; stem cell antigen; SCAH-1; SCAH-2; THP-1; bladder tumour;

XX KW diagnosis; screening; sca-2; LY-6 family; leukaemia; cancer.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Protein 3..125

XX FT /label= SCAH-2

XX FT Misc-difference 96

XX FT /label= unknown

XX FT /note= "encoded by GSC"

XX PN W09800540-A1.

XX PD 08-JAN-1998.

XX PF 25-JUN-1997; 97WO-US10956.

XX PR 03-JUL-1996; 96US-0675508.

XX PA (INCY-) INCYTE PHARM INC.

XX

```
FI Au-Young J;
XX WPI; 1998-427478/36.
DR N-PSDB; AAV38045.
XX Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g.
PT diagnose and treat SCAH-1 or SCAH-2 related conditions such as
PT tumours and screen inhibitory compounds
XX Claim 16; Fig 2; 66pp; English.
XX The present sequence represents human stem cell antigen 2 (SCAH-2). SCAH
CC proteins can be administered therapeutically, e.g. to inhibit or reverse
CC the development of tumours. Antibodies to SCAH proteins can be used in
CC diagnostic tests for conditions associated with protein expression in
CC biological samples, by combining a sample with the antibody under
CC conditions suitable for antibody binding to the protein to form a
CC complex, and detecting the complex. Antibodies to SCAH-2 are especially
CC useful in diagnostic tests for conditions/diseases such as leukaemias or
CC malignant local tumours associated with SCAH-2 expression. SCAH-1 and
CC SCAH-2 have homology to Sca-2 and other stem cell antigens, and have
CC characteristics of the Ly-6 family of cysteine rich proteins. The
CC functional similarities among Ly-6 family proteins previously reported,
CC and the expression of SCAH-1 and SCAH-2 in tumours from several tissues
CC (e.g. breast, lung, bladder) indicated that SCAH proteins may be useful
CC as anticancer agents; SCAH antibodies, antagonists or inhibitors
CC identified using the proteins could also be useful in anticancer
CC treatments and to intervene in alloresponses associated with transplant
CC rejection and autoimmune diseases e.g. lupus nephritis. The nucleic acid
CC sequences encoding SCAH proteins are also useful therapeutically to
CC treat, e.g. leukaemias and cancers of the bladder or breast.
XX Sequence 125 AA;
SQ
Query Match 99.2%; Score 122; DB 19; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.5e-107;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCQTOLGECQWTARIRAVGLLT 60
Db 3 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCQTOLGECQWTARIRAVGLLT 62
Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCKNSGAHALQPAALILALPALGLLLWGP 120
Db 63 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCKNSGAHALQPAALILALPALGLLLWGP 122
Qy 121 GQL 123
Db 123 GQL 125
RESULT 2
AAW70522
ID AAW70522 standard; Protein; 123 AA.
XX AC AAW70522;
XX 02-FEB-1999 (first entry)
XX Human prostate stem cell antigen (PSCA).
XX Prostate stem cell antigen; PSCA; human; prostate cancer;
XX diagnosis; therapy; vaccine; antibody.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 50..64
XX FT /note= "claimed fragment (Claim 5)"
XX Peptide 71..82
XX FT /note= "claimed fragment (Claim 6)"
XX WO9840403-A1.
XX PN

XX 17-SEP-1998.
XX PD
XX 10-MAR-1998; 98WO-US04665.
XX PF
XX 13-FEB-1998; 98US-0074675.
XX PR
XX 10-MAR-1997; 97US-0814279.
XX PR
XX 12-JAN-1998; 98US-0071141.
XX XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Reiter R, Witte O;
XX PI
XX WPI; 1998-520801/44.
XX DR
XX N-PSDB; AAV33691.
XX
XX New prostate stem cell antigen protein, PSCA - useful in diagnosis
PT and treatment of prostate cancer, e.g. to produce vaccines or
PT generate antibodies for use in assays or therapeutically
XX Claim 2; Fig 1B; 63pp; English.
XX This polypeptide comprises a novel human prostate-specific cell
CC surface antigen (PSCA) that is widely over-expressed across all
CC stages of prostate cancer, including high grade prostate
CC intraepithelial neoplasia and androgen-dependent and -independent
CC prostate tumours. The amino acid sequence was deduced from
CC isolated cDNA clones (see AAV33691), and contains the highly
CC conserved cysteine residues of the Ly-6/Thy-1 gene family, as well
CC as showing homology to GPI-anchored proteins. PSCA proteins may be
CC used as diagnostic and/or prognostic markers of prostate cancer.
CC PSCA (or encoding nucleic acids) can also be used therapeutically
CC in vaccines, in assays to isolate ligands or other binding agents
CC and to produce antibodies. PSCA antibodies are useful in
CC diagnostic/prognostic assays to detect PSCA, e.g. to diagnose or
CC monitor the progress of prostate cancer in subjects. Claimed
CC immunoconjugates, including an antigen binding region (see
CC AAW70523-24) of the antibody and a toxin agent such as ricin, can be
CC used to selectively kill cells expressing PSCA antigens (claimed).
CC Host vector systems and a method of producing PSCA protein are
CC also claimed.
XX
SQ Sequence 123 AA;
Query Match 75.6%; Score 93; DB 19; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCQTOLGECQWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCQTOLGECQWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCKN 93
Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCKN 93
RESULT 3
AAW80956
ID AAW80956 standard; Protein; 123 AA.
XX AC AAW80956;
XX 16-MAR-1999 (first entry)
XX PS116 antigen.
XX Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
XX detection; therapy; prostate cancer; metastasis.
XX Homo sapiens.
XX WO9851805-A1.
XX PN
```

XX PD 19-NOV-1998.
XX XX
XX PF 15-MAY-1998; 98WO-US10041.
XX PR 15-MAY-1997; 97US-0856653.
XX PA (ABBO) ABBOTT LAB.
XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-Rapp L, Russell JC, Stroupe SD;
XX DR WPI; 1999-045234/04.
XX XX
XX PT New method for detecting diseases of the prostate - comprises use of
PT a PS116 polynucleotide, protein or antibodies, useful for preventing
PT and treating prostate infections and cancer
XX PS Claim 17; Page 97; 118pp; English.
XX CC This sequence represents a PS116 antigen. The PS116 gene sequences were
CC isolated as expressed sequence tag (EST) clone of the PS116 gene isolated
CC from a human prostate tissue library. The PS116 sequences can be used in
CC the method of the invention for detecting a target PS116 polynucleotide
CC (PN), that comprises: contacting a sample with at least 1 PS116-specific
CC PN or complement; and detecting the target PS116 PN, where the specific
CC PN has at least 50% identity with the PS116 sequences. The PNs, PS116
CC polypeptides (such as this sequence) or PS116 amplicons are used to
CC detect prostate disease. Antibodies (Abs) against PS116 are used in assay
CC kits to detect PS116 antigen or anti-PS116 Ab, and the Abs are preferably
CC attached to a solid phase. The polypeptides are used for detecting
CC PS116-specific Abs in a sample, and for producing Abs after immunising a
CC subject. Plasmids encoding PS116 epitopes can also be administered to a
CC subject to obtain Abs. The cDNAs and polypeptides are useful for
CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
CC imaging, preventing, treating or determining the predisposition of a
CC subject to diseases and conditions of the prostate, such as prostate
CC cancer. The Abs and agonists or inhibitors are useful for treating
CC prostate diseases, tumours and metastases.
XX XX
SQ Sequence 123 AA;
Query Match 75.6%; Score 93; DB 20; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCITQGEQCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCITQGEQCWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLN 93
Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLN 93
RESULT 4
AAW86024
ID AAW86024 standard; Protein; 123 AA.
AC AAW86024;
XX XX
XX DT 23-FEB-1999 (first entry)
XX DE UT116 polypeptide consensus sequence.
XX KW UT116; urinary tract; epitope; antigen; detection; diagnosing;
KW monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
KW metastasis.
XX XX
OS Homo sapiens.
XX W09851824-A1.
PN

XX PD 19-NOV-1998.
XX XX
XX PF 15-MAY-1998; 98WO-US09972.
XX PR 15-MAY-1997; 97US-0856652.
XX PA (ABBO) ABBOTT LAB.
XX PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD;
PI Roberts-rapp L, Russell JC, Stroupe SD;
XX DR WPI; 1999-045237/04.
XX DR N-PSDB; AAV80396, AAV80397.
XX XX
XX PT New method for detecting diseases of the urinary tract - comprises
PT use of a UT116 polynucleotide, protein or antibodies, used for
PT preventing and treating urinary tract infections and cancer
XX PS Claim 10; Page 94; 113pp; English.
XX CC This represents the consensus sequence of the UT116 polypeptide, derived
CC from urinary tract tissue. The invention relates to a method of
CC detecting the presence of a target UT116 polynucleotide in a test sample
CC using UT116 gene-specific sequences (AAV80386 to AAV80397). Host cells
CC transfected with an expression vector containing the UT116 gene can be
CC used to produce a UT116 polypeptide recombinantly. This polypeptide has
CC at least one UT116 epitope which can be used in a method for detecting
CC UT116 antigen in a test sample. The polynucleotides and polypeptides are
CC useful for detecting, diagnosing, monitoring, staging, prognosticating,
CC in vivo imaging, preventing, treating or determining the predisposition
CC of a subject to diseases and conditions of the urinary tract, such as
CC urinary tract cancer. Antibodies specifically binding to an epitope of
CC UT116 antigen, and agonists are useful for treating urinary tract
CC diseases, tumours and metastases.
XX XX
SQ Sequence 123 AA;
Query Match 75.6%; Score 93; DB 20; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCITQGEQCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCAKQVSNEDCLQVENCITQGEQCWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLN 93
Db 61 VISKGSCLNCVDDSDQYVVGKKNITCCDIDLN 93
RESULT 5
AAV99707
ID AAV99707 standard; Protein; 123 AA.
XX XX
XX AC AAV99707;
XX XX
XX DT 07-SEP-2000 (first entry)
XX XX Human prostate stem cell antigen, PSCA.
XX DE Human; prostate cancer; prostate stem cell antigen; PSCA;
KW chromosome 8q24.2; bladder cancer; anti-apoptosis; proliferation;
KW GPI-anchored cell surface antigen; glycosylphosphatidylinositol.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
FT Peptide 1..20
FT Misc-difference 1 /label= signal_peptide
FT /note= "Encoded by GTG"

```

FT Protein- 21..123
FT /label= Mature_protein
FT Modified-site 32
FT /note= "N-glycosylated"
FT Modified-site 40
FT /note= "N-glycosylated"
FT Misc-difference 74
FT /note= "Encoded by TTA"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 93
FT /note= "N-glycosylated"
FT Region 100..123
FT /label= GPI-anchoring_sequence
XX
XX WO200032752-A1.
XX
XX 08-JUN-2000.
XX
XX 02-DEC-1999; 99WO-US28883.
XX
XX 02-DEC-1998; 98US-0203939.
XX
XX 17-FEB-1999; 99US-0251835.
XX
XX 25-MAY-1999; 99US-0318503.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX
XX Reiter R, Witte O;
XX
XX WPI; 2000-412305/35.
XX
XX N-PSDB; AAA48374.
XX
XX Prostate stem cell antigens, the nucleic acids encoding them and
XX antibodies against them, useful for diagnosing and treating prostate
XX cancer, bladder carcinomas and/or bone metastases of prostate cancer -
XX
XX Claim 18; Fig 1; 171pp; English.
XX
XX
XX The present sequence is the human Prostate Stem Cell Antigen (PSCA).
XX PSCA is a glycosylphosphatidylinositol (GPI)-anchored cell surface
XX antigen, which is expressed across a variety of normal cells: prostate
XX cells, urothelium, renal collecting ducts, colonic neuroendocrine cells,
XX placenta, bladder and ureteral transitional epithelial cells. However,
XX PSCA is widely over-expressed across all stages of prostate cancer,
XX including high grade prostatic intraepithelial neoplasia (PIN),
XX androgen-dependent and androgen-independent prostate tumours and bladder
XX carcinoma. The expression of PSCA appears to correlate with increasing
XX grade and so PSCA may be used as a prostate cancer marker, to
XX discriminate between malignant prostate cancers, normal prostate glands
XX and non-malignant neoplasias. It is hypothesised that PSCA may play a
XX role in stem/progenitor cell function such as self-renewal
XX (anti-apoptosis) and/ or proliferation. The PSCA gene has been localised
XX to chromosome 8q24.2. Fragments of the present sequence (AA99712,
XX AA99713 and AA99714) may be used as antigens to produce antibodies
XX against PSCA. The antibodies may then be used to detect and quantify the
XX presence of PSCA proteins in samples and hence diagnose and prognose
XX prostate cancer. The antibodies may also be used in the treatment of
XX cancers associated with PSCA by inhibiting its expression.
XX
XX Sequence 123 AA;
XX
XX Query Match 75.6%; Score 93; DB 21; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-79;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCITQIGQCWTARIVAGLLT 60
XX
XX 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCITQIGQCWTARIVAGLLT 60
XX
XX 61 VISKGCINCVDSDQDYVVGKKNITCCDIDL 93
XX
XX 61 VISKGCINCVDSDQDYVVGKKNITCCDIDL 93

```

```

RESULT 6
AAE03746
ID AAE03746 standard; Protein; 123 AA.
XX
XX AAE03746;
XX
XX 07-AUG-2001 (first entry)
XX
XX Human prostate stem cell antigen (PSCA) protein.
XX
XX Human; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
XX glycoprotein; cancer; prostate; bladder; lung; tumour.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= Signal_peptide
XX Protein 21..123
XX /label= Mature_human_PSCA_protein
XX Region 21..100
XX /note= "C-terminal GPI-anchoring sequence"
XX
XX WO200140309-A2.
XX
XX 07-JUN-2001.
XX
XX 27-OCT-2000; 2000WO-US29603.
XX
XX 29-OCT-1999; 99US-0162558.
XX
XX 16-FEB-2000; 2000US-0182872.
XX
XX (GETH ) GENENTECH INC.
XX
XX Devaux B, Keller G, Koeppe H, Lasky LA;
XX
XX WPI; 2001-389954/41.
XX
XX N-PSDB; AAD08171.
XX
XX Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
XX on binding to PSCA on mammalian cell and inhibits growth of
XX PSCA-expressing cancer cells in vivo, useful for killing
XX PSCA-expressing cancer cells -
XX
XX Example 1; Fig 17; 112pp; English.
XX
XX The present sequence is human prostate stem cell antigen (PSCA).
XX PSCA is a single subunit glycoprotein that is expressed on the
XX cell surface as a glycosylphosphatidylinositol (GPI)-anchored
XX protein. The present invention relates to anti-PSCA antibody composition
XX and methods of killing PSCA-expressing cancer cells. PSCA is useful for
XX inhibiting and killing the growth of PSCA-expressing cancer cells such as
XX prostate cancer, bladder cancer or lung cancer cells. Humanised antibody
XX conjugated to a toxin or a radioactive isotope is used for killing the
XX cancer cells. PSCA is useful for specifically targeting PSCA-expressing
XX tumour cells in vivo and for inhibiting or killing these cells. The
XX antibodies are also useful for treating the above mentioned cancers and
XX for diagnosing and staging of PSCA-expressing cancer, for purification
XX or immunoprecipitation of PSCA from cells, and for detection and
XX quantitation of PSCA in vitro. PSCA DNA is also useful for treating
XX cancers by gene therapy techniques.
XX
XX Sequence 123 AA;
XX
XX Query Match 75.6%; Score 93; DB 22; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-79;
XX Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCITQIGQCWTARIVAGLLT 60
XX
XX 1 MKAVLLALLMAGLALPGTALLCYSCKAQVSNEDCLQVENCITQIGQCWTARIVAGLLT 60
XX
XX 61 VISKGCINCVDSDQDYVVGKKNITCCDIDL 93
XX
XX 61 VISKGCINCVDSDQDYVVGKKNITCCDIDL 93

```

QY 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCLN 93
 Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCLN 93

RESULT 7
 AAU76692
 ID AAU76692 standard; Protein; 123 AA.
 AC AAU76692;
 XX
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human prostate stem cell antigen (PSCA) protein sequence.
 XX
 KW Human; prostate stem cell antigen; PSCA; antibody; immunogen;
 KW prostate cancer; bladder cancer; pancreatic cancer; immunconjugate;
 KW PSCA-associated cancer; PSCA antigen.
 XX
 OS Homo sapiens.
 XX
 XX
 PN US2001055751-A1.
 XX
 XX
 PD 27-DEC-2001.
 XX
 XX
 PF 03-MAY-2000; 2000US-0564329.
 XX
 XX
 PR 10-MAR-1997; 97US-228816P.
 PR 12-JAN-1998; 98US-071141P.
 PR 13-FEB-1998; 98US-074675P.
 PR 21-DEC-1998; 98US-113230P.
 PR 17-FEB-1999; 99US-120536P.
 PR 16-MAR-1999; 99US-124658P.
 PR 10-MAR-1998; 98US-0038261.
 PR 02-DEC-1998; 98US-0203939.
 PR 17-FEB-1999; 99US-0251835.
 PR 25-MAY-1999; 99US-0318503.
 PR 20-JUL-1999; 99US-0359326.
 XX
 PA (REIT/) REITER R E.
 PA (WITTE/) WITTE O N.
 PA (SAFF/) SAFFRAN D C.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Reiter RE, Witte ON, Saffran DC, Jakobovits A;
 XX
 XX WPI: 2002-194864/25.
 DR N-PSDB; ABK09980.
 XX
 PT New antibodies specifically binding a novel prostate cell surface
 PT antigen, PSCA, useful as antitumour agents in treatment of prostate,
 PT bladder and pancreatic cancer and in prostate cancer diagnosis
 XX
 PS Example 1; Fig 1b; 127pp; English.

CC The present invention relates to new antibodies that specifically bind a
 CC novel prostate stem cell antigen (PSCA), which is widely over-expressed
 CC across all stages of prostate cancer. The antibodies of the invention
 CC are useful to kill tumour cells expressing PSCA and as PSCA expression is
 CC observed in prostate tumour cells and in other human cancers,
 CC particularly bladder and pancreatic carcinomas, the antibodies are
 CC useful therapeutically to treat these diseases. In particular, monoclonal
 CC antibodies can be administered to subjects suffering from PSCA-associated
 CC cancers, e.g. prostate, bladder or pancreatic cancer or metastatic
 CC prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong
 CC the subject's life. The antibodies can be combined with a therapeutic
 CC agent in immunoconjugates useful to treat subjects suffering from
 CC malignant diseases, characterised by cells having PSCA antigen on the
 CC cell surface e.g. cancers, by killing the cells. The antibodies and
 CC immunoconjugates may also be included with a carrier in pharmaceutical
 CC compositions useful to kill human cells expressing PSCA antigen on the
 CC cell surface. The antibodies are also useful diagnostically to detect
 CC cancers, especially prostate cancer, to isolate prostate cancer cells

CC e.g. to enable culture growth to evaluate candidate therapeutic
 CC compounds, assist in identification of rare genes associated with
 CC prostate cancer, and to isolate and purify PSCA and PSCA homologues.
 CC The present amino acid sequence represents the human prostate stem cell
 CC antigen (PSCA) protein of the invention.

QY 1 MKAVLLALLMAGLALOPGTALLCYSCAKQVSNEDCLQVENCITOLGECQWTARAVGLLT 60
 Db 1 MKAVLLALLMAGLALOPGTALLCYSCAKQVSNEDCLQVENCITOLGECQWTARAVGLLT 60
 QY 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCLN 93
 Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLCLN 93

Query Match 75.6%; Score 93; DB 23; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.2e-79;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 ABR48224
 ID ABR48224 standard; Protein; 123 AA.
 XX
 AC ABR48224;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Human bladder cancer associated protein sequence SEQ ID NO:169.
 XX
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX W02003003906-A2.
 PN 16-JAN-2003.
 PD
 XX
 XX 03-JUL-2002; 2002WO-US21338.
 PF
 XX
 PR 03-JUL-2001; 2001US-302814P.
 PR 03-AUG-2001; 2001US-310099P.
 PR 08-NOV-2001; 2001US-343705P.
 PR 13-NOV-2001; 2001US-350666P.
 PR 12-APR-2002; 2002US-372246P.
 PR
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA
 XX Mack DH, Aziz N;
 PI
 XX WPI: 2003-201532/19.
 DR N-PSDB; ACC51040.
 DR
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with
 PT a bladder cancer-associated polynucleotide or antibody
 XX
 PS Claim 10; Page 288; 307pp; English.

CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in

CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications.

SQ Sequence 123 AA;

Query Match 75.6%; Score 93; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLNC 93
Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLNC 93

RESULT 9

ABP74203
ID ABP74203 standard; Protein; 123 AA.

AC ABP74203;

XX 03-FEB-2003 (first entry)

XX Human PSCA protein SEQ ID NO:79.

XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KW T cell.

XX Homo sapiens.

XX WO200281646-A2.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-US11101.

XX 06-APR-2001; 2001US-282211P.

XX 07-NOV-2001; 2001US-337017P.

XX 07-MAR-2002; 2002US-363210P.

XX (CTL1-) CTL IMMUNOTHERAPIES CORP.

XX Sinard JLL, Diamond DC, Liu L, Xie Z;

XX WPI; 2003-067518/06.

XX N-PSDB; ABQ83853.

XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
PT encoding the peptides, that are useful epitopes of target-associated
PT antigens -

PS Claim 1; Page 164; 352pp; English.

XX The present invention describes an isolated epitope (I) and an epitope
CC cluster. Also described is a vaccine or immunotherapeutic composition
CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
CC treating an animal, by administering to an animal the vaccine or
CC immunotherapeutic composition. VC is also useful for evaluating
CC immunogenicity of a vaccine or immunotherapeutic composition, by
CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74713 represent sequences used in the exemplification of the present
CC invention.

XX Sequence 123 AA;

Query Match 75.6%; Score 93; DB 24; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLLT 60
Db 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLLT 60
Qy 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLNC 93
Db 61 VISKGSCLNCVDDSDQDYVVGKKNITCCDIDLNC 93

RESULT 10

AAB35285
ID AAB35285 standard; Protein; 123 AA.

XX AAB35285;

XX 08-MAY-2001 (first entry)

XX Human prostate stem cell antigen.

XX Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
KW diagnosis; treatment; chromosome 8q24.2.

XX Homo sapiens.

XX WO200105427-A1.

XX 25-JAN-2001.

XX 20-JUL-2000; 2000WO-US19967.

XX 20-JUL-1999; 99US-0359326.

XX 03-MAY-2000; 2000US-0564329.

XX (REGC) UNIV CALIFORNIA.

XX (UROG-) UROGENESYS.

XX Reiter R, Witte O, Saffran DC, Jakobovits A;

XX WPI; 2001-159478/16.

XX N-PSDB; AAF27971.

XX Antibodies binding to prostate stem cell antigen inhibit the growth of
PT cancer cells and are used to detect and treat prostate, pancreatic or
PT bladder cancers -

PS Example 1; Fig 1B; 229pp; English.

XX The present invention describes a method of treating cancer associated
CC with prostate stem cell antigen (PSCA) by administering an antibody which
CC selectively binds to PSCA and inhibits the growth of the cancer cells.
CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
CC the human and murine PSCA protein and coding sequences, which can be used
CC not only in the treatment of, but also in detection and prognosis of
CC prostate cancer.

XX Sequence 123 AA;

Query Match 74.0%; Score 91; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 9.4e-78;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLTVI 62
Db 3 AVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCCTOLGEOCWTARIRAVGLTVI 62

Qy 63 SKGCSLNCVDDSDQDYVVGKKNITCCDIDLNC 93

Db 63 SKGCSLNCVDDSDQDYVVGKKNITCCDIDLNC 93


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PR 31-OCT-1997; 97US-0063870.
PR 31-OCT-1997; 97US-0064103.
PR 03-NOV-1997; 97US-0064248.
PR 07-NOV-1997; 97US-0064809.
PR 12-NOV-1997; 97US-0065186.
PR 17-NOV-1997; 97US-0065846.
PR 18-NOV-1997; 97US-0065693.
PR 21-NOV-1997; 97US-0066120.
PR 21-NOV-1997; 97US-0066364.
PR 24-NOV-1997; 97US-0066772.
PR 24-NOV-1997; 97US-0066466.
PR 24-NOV-1997; 97US-0066770.
PR 24-NOV-1997; 97US-0066511.
PR 24-NOV-1997; 97US-0066453.
PA (GETH ) GENENTECH INC.
XX
XX Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
XX WPI; 1999-229533/19.
XX N-PSDB; AAX52217.
XX
XX New isolated human genes and polypeptides used in, e.g. treatment of
XX gastrointestinal ulceration
XX
XX Claim 12; Fig 9; 320pp; English.
XX
XX AAY13344-403 represent secreted and transmembrane human proteins.
XX The cDNA sequences are obtained from cDNA libraries, prepared from
XX fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
XX The encoded polypeptides have specific uses based on their homology to
XX known polypeptides, e.g. PRO211 and PRO217 can be used for disorders
XX associated with the preservation and maintenance of gastrointestinal
XX mucosa and the repair of acute and chronic mucosal lesions
XX (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal
XX ulceration and congenital microvillus atrophy), skin diseases associated
XX with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial
XX cancers such as lung squamous cell carcinoma of the vulva and gliomas),
XX potent effects on cell growth and development, diseases related to
XX growth or survival of nerve cells including Parkinson's disease,
XX Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as
XX for fibronectin, e.g. for reducing dermal scarring. PRO264 can be used
XX as a target for anti-tumor drugs. PRO533 may be used in the treatment
XX of Usher Syndrome or Atrophia areata; PRO269 can be used as an
XX anti-thrombotic agent; PRO287 polypeptides and portions may have
XX therapeutic applications in wound healing and tissue repair; PRO317 can
XX be used for treating problems of the kidney, uterus, endometrium, blood
XX vessels, or related tissue, e.g. in the heart of genital tract.
XX
XX SQ Sequence 114 AA;
XX
XX Query Match 68.3%; Score 84; DB 20; Length 114;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-71;
XX Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 10 MAGLALPGTALLCYSCKAQVSNEDCLQVENCNTQLGEQCTARIRAVGLLTIVISKGCSLN 69
XX
XX 1 MAGLALPGTALLCYSCKAQVSNEDCLQVENCNTQLGEQCTARIRAVGLLTIVISKGCSLN 60
XX
XX 70 CVDDSDQYVVGKKNITCCDIDLN 93
XX
XX 61 CVDDSDQYVVGKKNITCCDIDLN 84
XX
XX
XX RESULT 13
XX AAY13938
XX ID AAY13938 standard; Protein; 123 AA.
XX
XX AC AAY13938;
XX
XX DT 14-JUL-1999 (first entry)
XX
XX DE Human transmembrane protein, HP01244.
XX
XX
XX Transmembrane protein; human; cell membrane; proliferation; diagnosis;
XX cell differentiation; carcinostatic agent; probe; gene therapy;
XX signal transduction; apoptosis; inhibitor;
XX phosphatidylethanolamine N-methyltransferase.
XX
XX Homo sapiens.
XX
XX WO9918203-A2.
XX
XX 15-APR-1999.
XX
XX 05-OCT-1998; 98WO-JP04475.
XX
XX 08-OCT-1997; 97JP-0276271.
XX
XX (PROT-) PROTEGENE INC.
XX (SAGA ) SAGAMI CHEM RES CENT.
XX
XX Kato S, Kobayashi M, Sekine S, Yamaguchi T;
XX WPI; 1999-277268/23.
XX N-PSDB; AAX36800, AAX36801.
XX
XX Human transmembrane proteins and nucleotide sequences
XX
XX Claim 1; Page 82-83; 139pp; English.
XX
XX This sequence is a human transmembrane protein of the invention.
XX All of the proteins exist in the cell membrane, so are considered to be
XX proteins controlling the proliferation and differentiation of the cells.
XX They may be useful as carcinostatic agents or as antigens for preparing
XX antibodies against the proteins. The cDNAs can be used as probes for
XX gene diagnosis and gene sources for gene therapy, as well as for
XX large-scale expression of the proteins. The HP01498 (see AAY13939)
XX protein may be associated with signal transduction associated with
XX apoptosis, and therefore useful in inhibition of apoptosis. The HP01962
XX (see AAY13943) protein can be used to treat diseases associated with
XX phosphatidylethanolamine N-methyltransferase. The proteins are
XX identified by the presence of a hydrophobic transmembrane region.
XX Knowledge of the protein function is not required, as in e.g. methods of
XX expression cloning.
XX
XX SQ Sequence 123 AA;
XX
XX Query Match 43.9%; Score 54; DB 20; Length 123;
XX Best Local Similarity 100.0%; Pred. No. 6.2e-43;
XX Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 40 NCTQLGEQCTARIRAVGLLTIVISKGCSLNCVDDSDQYVVGKKNITCCDIDLN 93
XX
XX 40 NCTQLGEQCTARIRAVGLLTIVISKGCSLNCVDDSDQYVVGKKNITCCDIDLN 93
XX
XX
XX RESULT 14
XX ABB11977
XX ID ABB11977 standard; peptide; 117 AA.
XX
XX AC ABB11977;
XX
XX DT 11-JAN-2002 (first entry)
XX
XX DE Human stem cell Ag homologue, SEQ ID NO:2347.
XX
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
XX haematopoiesis regulation; tissue growth; immunomodulator; activin;
XX inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
XX proliferation; metastasis; cancer; tumour; haematopoietic disorder;
XX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
XX chronic inflammatory condition; proliferative retinopathy;
XX atherosclerosis; coronary heart disease; arterial ischaemia;
XX bone disorder; osteoporosis; vascular growth disorder;
XX tissue regeneration; wound healing; infection; immune disorder;

```

KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytotatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.
 XX Homo sapiens.
 PN WO200157188-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US03800.
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX WPI; 2001-457740/49.
 DR N-PSDB; ABA09221.
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX Claim 20; Page 291; 1963pp; English.
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

XX Sequence 117 AA;

Query Match 41.5%; Score 51; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.9e-40;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLLALLMAGIALQPGTALLCYSCKAQVSNEDCLQVENCNTOLGEOCWHTARIR 54
 Db 58 VLLALLMAGIALQPGTALLCYSCKAQVSNEDCLQVENCNTOLGEOCWHTARIR 108
 RESULT 15
 AAW80958
 ID AAW80958 standard; Protein; 41 AA.
 XX
 AC AAW80958;
 XX
 DT 16-MAR-1999 (first entry)
 XX
 DE PS116 antigen.
 XX
 KW Human; expressed sequence tag; EST; prostate disease; diagnosis; tumour;
 KW detection; therapy; prostate cancer; metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO9851805-A1.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US10041.
 XX
 PR 15-MAY-1997; 97US-0856653.
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-Rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI; 1999-045234/04.
 XX
 PT New method for detecting diseases of the prostate - comprises use of
 PT a PS116 polynucleotide, protein or antibodies, useful for preventing
 PT and treating prostate infections and cancer
 XX
 PS Claim 17; Page 98; 118pp; English.
 CC
 CC This sequence represents a PS116 antigen. The PS116 gene sequences were
 CC isolated as expressed sequence tag (EST) clone of the PS116 gene isolated
 CC from a human prostate tissue library. The PS116 sequences can be used in
 CC the method of the invention for detecting a target PS116 polynucleotide
 CC (PN), that comprises: contacting a sample with at least 1 PS116-specific
 CC PN or complement; and detecting the target PS116 PN, where the specific
 CC PN has at least 50% identity with the PS116 sequences. The PNs, PS116
 CC polypeptides (such as this sequence) or PS116 amplicons are used to
 CC detect prostate disease. Antibodies (Abs) against PS116 are used in assay
 CC kits to detect PS116 antigen or anti-PS116 Ab, and the Abs are preferably
 CC attached to a solid phase. The polypeptides are used for detecting a
 CC PS116-specific Abs in a sample, and for producing Abs after immunising a
 CC subject. Plasmids encoding PS116 epitopes can also be administered to a
 CC subject to obtain Abs. The cDNAs and polypeptides are useful for
 CC detecting, diagnosing, staging, monitoring, prognosticating, in vivo
 CC imaging, preventing, treating or determining the predisposition of a
 CC subject to diseases and conditions of the prostate, such as prostate
 CC cancer. The Abs and agonists or inhibitors are useful for treating
 CC prostate diseases, tumours and metastases.
 XX
 SQ Sequence 41 AA;

Query Match 33.3%; Score 41; DB 20; Length 41;
 Best Local Similarity 100.0%; Pred. No. 3.9e-31;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 RIRAVGLLTIVISKGSLNCVDDSDQDYVVGKKNITCCDTDLIC 92
 Db 1 RIRAVGLLTIVISKGSLNCVDDSDQDYVVGKKNITCCDTDLIC 41

Search completed: August 18, 2003, 19:54:27
Job time : 84 secs